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STIC-Biotech/ChemLib

89679

From: Monshipouri, Maryam
Sent: Monday, March 24, 2003 9:47 AM
To: STIC-Biotech/ChemLib
Subject: case #09/719,748

Please **interference** search SEQ ID NO:1-2,
residues 1022-1141 of SEQ ID NO:1 ;and
residues 13-275 of SEQ ID NO:2.

Thank you.

Maryam Monshipouri Ph.D.
Primary Examiner
Art Unit 1652
Mail box No. 10D01

Point of Contact
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

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Monshypour
09/17/19748
Seq. IDs 172 (Interf

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 19:24:37 ; Search time 5382.24 Seconds
(without alignments)
8137.548 Million cell updates/sec

Title: US-09-719-748-1

Perfect score: 1742

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

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| 3 | 1742 | 100.0 | 1742 | 1 PCT-US99-13411-1 | Sequence 1, Appl1 |
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| 5 | 1728.8 | 99.2 | 2235 | US-09-649-163-9855 | Sequence 9895, Ap |
| 6 | 1728.8 | 99.2 | 2235 | US-09-652-917-3775 | Sequence 3775, Ap |
| 7 | 1728.8 | 99.2 | 2235 | US-09-652-917-3775 | Sequence 12235, A |
| 8 | 1728.8 | 99.2 | 2235 | US-09-652-917-3775 | Sequence 6041, Ap |
| 9 | 1715.8 | 98.5 | 1970 | US-09-698-010-12235 | Sequence 3329, Ap |
| 10 | 1042.2 | 59.8 | 1864 | US-09-278-232-31329 | Sequence 10, Appl |
| 11 | 1032.4 | 59.3 | 1732 | US-09-360-207-7361 | Sequence 3361, Ap |
| 12 | 1019.2 | 58.5 | 1512 | US-09-449-163-7647 | Sequence 7647, Ap |
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| 18 | 1015 | 58.3 | 1253 | PCT-US01-08631-9265 | Sequence 8371, Ap |
| 19 | 952 | 54.6 | 1198 | US-09-652-914-8371 | Sequence 450, App |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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45 517.2 29.7 2387 27 US-09-659-999-6197 Sequence 6197, App

ALIGNMENTS

RESULT 1
PCT-US99-13411-1
Sequence 1, Application PC/TUS9913411

GENERAL INFORMATION:
APPLICANT: KIMCHI, Adi
APPLICANT: MCINNIS A., Patricia
APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
FILE REFERENCE: KIMCHI2
CURRENT APPLICATION NUMBER: PCT/US99/13411
CURRENT FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,294
EARLIER FILING DATE: 1998-06-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1742
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (62)..(1141)
PCT-US99-13411-1

Query Match 100.0%; Score 1742; DB 1; Length 1742;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

PCT-US99-13411-1

Sequence 1, Application PC/TUS9913411A
GENERAL INFORMATION:
APPLICANT: KIMCHI, Adi
APPLICANT: MCINNIS A., Patricia
APPLICANT: YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.
TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
FILE REFERENCE: KIMCHI2A
CURRENT APPLICATION NUMBER: PCT/US99/13411A
CURRENT FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,294
EARLIER FILING DATE: 1998-06-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1742
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (62) .. (1141)
PCT-US99-13411-1

Query Match 100.0%; Score 1742; DB 1; Length 1742;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1741 AA 1742
Db 1741 AA 1742

RESULT 3
US-09-719-748-1
; Sequence 1, Application US/09719748
; GENERAL INFORMATION:
; APPLICANT: KIMCHI, Adi
; TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
; FILE REFERENCE: KIMCHI2A
; CURRENT APPLICATION NUMBER: US/09/719,748
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/089,294
; PRIOR FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (62)...(1141)
US-09-719-748-1

Query Match 100.0%; Score 1742; DB 28; Length 1742;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1742; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACGCGGAGCTCAGGCTCCGCGAATGTATGTTCCAGGCTTCAATGAGAGTCCAA 60
Db 1 GACGCGGAGCTCAGGCTCCGCGAATGTATGTTCCAGGCTTCAATGAGAGTCCAA 60
QY 61 CATGAGCATTTCAAGCAAGAAAGTGAAGACTTTTATGATCGAGAGAGCTGGG 120
Db 61 CATGAGCATTTCAAGCAAGAAAGTGAAGACTTTTATGATCGAGAGAGCTGGG 120
QY 121 GAGTGGCAATTTGCTCATCTGTGAAGAGTGCCTGGAGAGAGCAAGGAGCTTGAATGC 180
Db 121 GAGTGGCAATTTGCTCATCTGTGAAGAGTGCCTGGAGAGAGCAAGGAGCTTGAATGC 180

QY 181 AGCGAATTCATCAAGAAAGCGGAGAGCGGCGAGCCTGGCGGTGTGAGCCGGAGGA 240
Db 181 AGCGAATTCATCAAGAAAGCGGAGAGCGGCGAGCCTGGCGGTGTGAGCCGGAGGA 240
QY 241 GATGAGCGGAGGTGAGCATCTCGCGGAGGTGTGACCAAAATGTCATCAGCTGCA 300
Db 241 GATGAGCGGAGGTGAGCATCTCGCGGAGGTGTGACCAAAATGTCATCAGCTGCA 300
QY 301 GAGCTCTAATGAAGAACCGACCGAGCTGTGACATCTTGAAGTGTGTGAGAGGA 360
Db 301 GAGCTCTAATGAAGAACCGACCGAGCTGTGACATCTTGAAGTGTGTGAGAGGA 360
QY 361 GCTCTTCAATTTCTGCGCCAGAAAGAGTCACTGAGTGAAGAGGAGCCAGACTTCA 420
Db 361 GCTCTTCAATTTCTGCGCCAGAAAGAGTCACTGAGTGAAGAGGAGCCAGACTTCA 420
QY 421 TAAGAGATCTGATGAGGAGTGAATCTTCAACAAAGAAATTTGCTCACTTGAAT 480
Db 421 TAAGAGATCTGATGAGGAGTGAATCTTCAACAAAGAAATTTGCTCACTTGAAT 480
QY 481 CAAGCAGAAACATTAATGTTGTTAGCAAGAAATATTCATTCACATCAAGCTGAT 540
Db 481 CAAGCAGAAACATTAATGTTGTTAGCAAGAAATATTCATTCACATCAAGCTGAT 540
QY 541 TGACTTGTGTGCTGCTCAGAAATTAAGAGATGAGTTGAATTTAAGAAATTTTGGAC 600
Db 541 TGACTTGTGTGCTGCTCAGAAATTAAGAGATGAGTTGAATTTAAGAAATTTTGGAC 600
QY 601 GCGGAAATTTGTTGCTCAGAAATTTGTAATGAGAGCTTGTGAGGCTGAGCAT 660
Db 601 GCGGAAATTTGTTGCTCAGAAATTTGTAATGAGAGCTTGTGAGGCTGAGCAT 660
QY 661 GTGAGCATAGCGGTGATCACTTCACTTCACTTGAAGTGAAGTGAAGTGAAGT 720
Db 661 GTGAGCATAGCGGTGATCACTTCACTTGAAGTGAAGTGAAGTGAAGTGAAGT 720
QY 721 CACGAAACGAAACACTGCAATATCAATGAGTGAAGTGAAGTGAAGTGAAGT 780
Db 721 CACGAAACGAAACACTGCAATATCAATGAGTGAAGTGAAGTGAAGTGAAGT 780
QY 781 CTTGAGCATATGAGGAGCTGCGCAAGGCTTATTTGGAAGCTTGTGTTAAAGAG 840
Db 781 CTTGAGCATATGAGGAGCTGCGCAAGGCTTATTTGGAAGCTTGTGTTAAAGAG 840
QY 841 CCGGAAACGCTCAGATCAAGAGGCTTCAAGCAACCTGTGATGAGCTGAGCA 900
Db 841 CCGGAAACGCTCAGATCAAGAGGCTTCAAGCAACCTGTGATGAGCTGAGCA 900
QY 901 CCAGCAACCATGAGTGCAGCGGAGTCTGTGTAATCTGAGAACTTCAAGAAAGTA 960
Db 901 CCAGCAACCATGAGTGCAGCGGAGTCTGTGTAATCTGAGAACTTCAAGAAAGTA 960
QY 961 TGTCCGAGCGGTGAGAGCTTCTTCAAGCATGCTGCTGTGCAACCACTCACCC 1020
Db 961 TGTCCGAGCGGTGAGAGCTTCTTCAAGCATGCTGCTGTGCAACCACTCACCC 1020
QY 1021 CTGCTGATGAAGAAAGTGCACCTGAGGCTGAGTGAAGCACTTGAAGAGTA 1080
Db 1021 CTGCTGATGAAGAAAGTGCACCTGAGGCTGAGTGAAGCACTTGAAGAGTA 1080
QY 1081 CACTGAGAGGACATGCGCAGAGAGAAAGCCTTCAACCAAGAGAGAGCAGACCTC 1140
Db 1081 CACTGAGAGGACATGCGCAGAGAGAAAGCCTTCAACCAAGAGAGAGCAGACCTC 1140
QY 1141 CTAACTGAGCTGACCTGAGTGCAGTGGCGCGCAGGAGGTTTGGGCGGAGCTTCT 1200
Db 1141 CTAACTGAGCTGACCTGAGTGGCGCGCAGGAGGTTTGGGCGGAGCTTCT 1200
QY 1201 GTGAGCATTTTGAAGCCAGCTCAGACCAAGCAGGAGCTTGAAGCACTTGAAGA 1260
Db 1201 GTGAGCATTTTGAAGCCAGCTCAGACCAAGCAGGAGCTTGAAGCACTTGAAGA 1260
QY 1261 GAGATGGGCCAAGGAATTCAGAAAGCTTGCAGGCAAGCCAGAGACCTTGGAGCTGT 1320

|||||
Db 1261 GAGATGGGCCCCAAGAAATTCAGAAAGCTTGAAGCAAGCCAGAGGACCTGGGAGCTGT 1320
|||
Qy 1321 GGCCTCTTCTGTGGAGAGGCTCCAGCATTCCTTAAATTCCTCAATAATGG 1380
|||
Db 1321 GGCCTCTTCTGTGGAGAGGCTCCAGCATTCCTTAAATTCCTCAATAATGG 1380
|||
Qy 1381 GCTTTCCTCTGTCTGCATCTCAGAGTCTGGGAGTGTGTGACTTAAGAAAAAAT 1440
|||
Db 1381 GCTTTCCTCTGTCTGCATCTCAGAGTCTGGGAGTGTGTGACTTAAGAAAAAAT 1440
|||
Qy 1441 ATAAAGCATCTCTATCATCAAGGGGTGAAGGTCAAGTAAGGACCTTCTTACAGG 1500
|||
Db 1441 ATAAAGCATCTCTATCATCAAGGGGTGAAGGTCAAGTAAGGACCTTCTTACAGG 1500
|||
Qy 1501 CTGAGGGGGTTCAGAACAGAGCTGGCCAAAATTAACACAGAGAGAGAGCTCCCA 1560
|||
Db 1501 CTGAGGGGGTTCAGAACAGAGCTGGCCAAAATTAACACAGAGAGAGAGCTCCCA 1560
|||
Qy 1561 TTGGGAACAGGGGTGATTGAGAAAGTGAACCTTGGGTGTAGGGAACCAATCCTGTGACT 1620
|||
Db 1561 TTGGGAACAGGGGTGATTGAGAAAGTGAACCTTGGGTGTAGGGAACCAATCCTGTGACT 1620
|||
Qy 1621 CCCAGAACATGGAAGCCAGAGCTGAGCTGACCAACCTCAGACCTTCTGAAAGCAGC 1680
|||
Db 1621 CCCAGAACATGGAAGCCAGAGCTGAGCTGACCAACCTCAGACCTTCTGAAAGCAGC 1680
|||
Qy 1681 CCATTGCTGGCCGCGCATGTTGTATTTTGTGCTATTTTAACTTCTGGTTAACTCG 1740
|||
Db 1681 CCATTGCTGGCCGCGCATGTTGTATTTTGTGCTATTTTAACTTCTGGTTAACTCG 1740
|||
Qy 1741 AA 1742
|||
Db 1741 AA 1742

RESULT 4
US-09-606-776-3799
; Sequence 3799, Application US/09606776
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Myers, Paul
; APPLICANT: Geary, David P.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1129-001
; CURRENT APPLICATION NUMBER: US/09/606,776
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,578
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/141,379
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/141,138
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/141,581
; NUMBER OF SEQ ID NOS: 5415
; SOFTWARE: FaBSeq for Windows Version 3.0
; SEQ ID NO 3799
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-776-3799

Query Match 99.3%; Score 1730.4; DB 23; Length 2235;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1734; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ACCGGGAGGCTCAGGCTCCGCGGATGTTATGTTCCAGGCTCAATAGAGATGCCAAC 61
|||
Db 1 ACCGGGAGGCTCAGGCTCCGCGGATGTTATGTTCCAGGCTCAATAGAGATGCCAAC 60

Qy 62 ATGAGCCATTCAAGACAGAGAGGTGAGACTTTTATATGACATCGAGAGAGAGCTGGGG 121
|||
Db 61 ATGAGCCATTCAAGACAGAGAGAGGTGAGAGACTTTTATATGACATCGAGAGAGAGCTGGGG 120
|||
Qy 122 AGTGGCCAGTTTGGCATGTGTGAAGAGTCCGGGAGAGAACACAGGGGCTTGAATATCA 181
|||
Db 121 AGTGGCCAGTTTGGCATGTGTGAAGAGTCCGGGAGAGAACACAGGGGCTTGAATATCA 180
|||
Qy 182 GCCAAGTTCATCAAGAAAGCGGAGAGCCGGGCGAGCCGGGCGGTGTAGCCGGGAGAG 241
|||
Db 181 GCCAAGTTCATCAAGAAAGCGGAGAGCCGGGCGAGCCGGGCGGTGTAGCCGGGAGAG 240
|||
Qy 242 ATGAGCGGAGGTGAGCATCTGGGAGAGGTGTGACCACAATGTATCATCGCTGAC 301
|||
Db 241 ATGAGCGGAGGTGAGCATCTGGGAGAGGTGTGACCACAATGTATCATCGCTGAC 300
|||
Qy 302 GACGCTTATGAGAACCGGACCGGAGCTGTGACATCTTTAGCTTATGTCTGTGAGAGAG 361
|||
Db 301 GACGCTTATGAGAACCGGACCGGAGCTGTGACATCTTTAGCTTATGTCTGTGAGAGAG 360
|||
Qy 362 CTCTTCGATTTCTGGCCCAAGAGAGTCACTGAGTGAAGAGAGGACCAAGCTTCATT 421
|||
Db 361 CTCTTCGATTTCTGGCCCAAGAGAGTCACTGAGTGAAGAGAGGACCAAGCTTCATT 420
|||
Qy 422 AAGCAGATCTGATGAGGTGAACCTTCAACAAAGAAATTTCTCACTTGTATCTC 481
|||
Db 421 AAGCAGATCTGATGAGGTGAACCTTCAACAAAGAAATTTCTCACTTGTATCTC 480
|||
Qy 482 AAGCAGAAACATTTATTTGTGTAGCAAGAAATTTCCATTTCCACATCAAGCTGATT 541
|||
Db 481 AAGCAGAAACATTTATTTGTGTAGCAAGAAATTTCCATTTCCACATCAAGCTGATT 540
|||
Qy 542 GACTTGTGCTGGCTCAGCAATATGAGATGAGTGAATTTAAGAAATTTTGGAGC 601
|||
Db 541 GACTTGTGCTGGCTCAGCAATATGAGATGAGTGAATTTAAGAAATTTTGGAGC 600
|||
Qy 602 CCGGAATTTGTGCTCCAGAAATTTGTGAATGAGAGCCCTGGGTCTGAGAGCTGACATG 661
|||
Db 601 CCGGAATTTGTGCTCCAGAAATTTGTGAATGAGAGCCCTGGGTCTGAGAGCTGACATG 660
|||
Qy 662 TGGAGCATGGCTGATACCTACATCTCTTAAAGTGAAGATCCCTTTCTGGGAGAC 721
|||
Db 661 TGGAGCATGGCTGATACCTACATCTCTTAAAGTGAAGATCCCTTTCTGGGAGAC 720
|||
Qy 722 ACGAAGCAGAAACATGCGCAATATATCAATCAGAGTGTGACCTTGTATGAGGAATTC 781
|||
Db 721 ACGAAGCAGAAACATGCGCAATATATCAATCAGAGTGTGACCTTGTATGAGGAATTC 780
|||
Qy 782 TTCAGCCATACGAGAGCTGGCCAGAGACTTTTATGGAAGCTTCTGTTAAAGAGAC 841
|||
Db 781 TTCAGCCATACGAGAGCTGGCCAGAGACTTTTATGGAAGCTTCTGTTAAAGAGAC 840
|||
Qy 842 CGGAACCGCTCAATCAATCAAGAGCTTCAAGACCCCTTGATACGCGGTGAGAAC 901
|||
Db 841 CGGAACCGCTCAATCAATCAAGAGCTTCAAGACCCCTTGATACGCGGTGAGAAC 900
|||
Qy 902 CAGCAAGCATGATGCGAGCGGAGTGTGTGCAATCTGAGAACTTGAAGAGAGAT 961
|||
Db 901 CAGCAAGCATGATGCGAGCGGAGTGTGTGCAATCTGAGAACTTGAAGAGAGAT 960
|||
Qy 962 GTCCGAGCGGTGGAAGCTTCTTCAAGATCTGTCTCTGTGCAACCACTTCAAGAG 1021
|||
Db 961 GTCCGAGCGGTGGAAGCTTCTTCAAGATCTGTCTCTGTGCAACCACTTCAAGAG 1020
|||
Qy 1022 TCCGCTATGAAGAGTGCACCTTGAAGCCGATGAGACCTGAGAACTGTGAAGTAC 1081
|||
Db 1021 TCCGCTATGAAGAGTGCACCTTGAAGCCGATGAGACCTGAGAACTGTGAAGTAC 1080
|||
Qy 1082 ACTGAGAGGACATCGCAGGAGAGAAAGCCCTCAACCCAGGAGAGAGAGAGACCTCC 1141
|||
Db 1081 ACTGAGAGGACATCGCAGGAGAGAAAGCCCTCAACCCAGGAGAGAGAGAGACCTCC 1140
|||
Qy 1142 TAACTGGCTGACCTGACAGTGGCGCCAGGAGAGTTTGGGCCACAGCGGGGCTCTCTGTG 1201

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Db 1141 TAACTGCTTAACTGCTGAGTGGCCGACAGGAGGTCTGGGCCAGCGGGGCTCCCTTCTG 1200
Qy 1202 TGCAGACTTTTGGACCCAGCTTCAGACCAAGCAACCCGGGCGCTCCAGACACTTTTGCAGAG 1261
Db 1201 TGCAGACTTTTGGACCCAGCTTCAGACCAAGCAACCCGGGCGCTCCAGACACTTTTGCAGAG 1260
Qy 1262 AGATGGGGCCCAAGAAATTCAGAAAGCTTGCAGGCAACCCAGAGACCCCTGGAGCTGTG 1321
Db 1261 AGATGGGGCCCAAGAAATTCAGAAAGCTTGCAGGCAACCCAGAGACCCCTGGAGCTGTG 1320
Qy 1322 GCTGTCTTCTGTGAGAGAGCTCCAGCAATTCCTCAAAAGCTTTAATCTTCCATAAAAGAG 1381
Db 1321 GCTGTCTTCTGTGAGAGAGCTCCAGCAATTCCTCAAAAGCTTTAATCTTCCATAAAAGAG 1380
Qy 1382 CTTTCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1441
Db 1381 CTTTCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Qy 1442 TAAAGGACATCTCTCATCATCAAGGGGTGAAGGTCAAGAGTAAAGGCAAGCTTCTTCAAGGC 1501
Db 1441 TAAAGGACATCTCTCATCATCAAGGGGTGAAGGTCAAGAGTAAAGGCAAGCTTCTTCAAGGC 1500
Qy 1502 TGAAGGGGTTCAAGAACCAAGCTTGGCCCAAAATTAACAAGAGAGCAAGAGCTTCTTCAAGGC 1561
Db 1501 TGAAGGGGTTCAAGAACCAAGCTTGGCCCAAAATTAACAAGAGAGCAAGAGCTTCTTCAAGGC 1560
Qy 1562 TGGGAAACAGGGGTATTCAGAGAAAGTGAACCTTGGGTGTAGAGGAGCAACCTCTGTAGCCTC 1621
Db 1561 TGGGAAACAGGGGTATTCAGAGAAAGTGAACCTTGGGTGTAGAGGAGCAACCTCTGTAGCCTC 1620
Qy 1622 CCAGAACCATGAAAGCCAGAGACCTCAAGCTGACCAACCTCAAGCTTCTTGAAGAGCC 1681
Db 1621 CCAGAACCATGAAAGCCAGAGACCTCAAGCTGACCAACCTCAAGCTTCTTGAAGAGCC 1680
Qy 1682 CATTCGCGCGCCGCATGTTGTAATTTTGTCTATTTTATTAATTAACCTTGTGTTTACTGA 1741
Db 1681 CATTCGCGCGCCGCATGTTGTAATTTTGTCTATTTTATTAATTAACCTTGTGTTTACTGA 1740

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RESULT 5
US-09-649-163-9895
Sequence 9895, Application US/09649163

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GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Galvin, Katherine A.
APPLICANT: Leiby, Kevin R.
APPLICANT: Kingsbury, Gillian A.
APPLICANT: Weich, Nadine S.
APPLICANT: McCarthy, Sean A.
APPLICANT: Williamson, Mark
APPLICANT: Richardson, Jennifer
APPLICANT: MacBeth, Kyle J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Villaveal, Jean-Luc M.G.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Siles-Santlago, Inmaculada
APPLICANT: White, David
APPLICANT: Pan, Yang
APPLICANT: Buefield, Samantha J.
APPLICANT: Deeds, James
APPLICANT: Lee, John
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.1164-001
CURRENT APPLICATION NUMBER: US/09/649,163
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/150,608
NUMBER OF SEQ ID NOS: 10535
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9895

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; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-649-163-9895
Query Match 99.2%; Score 1728.8; DB 25; Length 2235;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1733; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 2 ACCGCGGAGCTCAGCTTCCGCGCATTTGATGTCAGAGCTCAATGAGAGTCCAAAC 61
Db 1 ACCGCGGAGCTCAGCTTCCGCGCATTTGATGTCAGAGCTCAATGAGAGTCCAAAC 60
Qy 62 ATGAGCCATTCAAGCAGAGAGGTGAGAGCTTTATGATCATGAGAGAGCTGGG 121
Db 61 ATGAGCCATTCAAGCAGAGAGGTGAGAGCTTTATGATCATGAGAGAGCTGGG 120
Qy 122 AGTGGCCAGTTGGCTCATCTGTAAAGATGCCGGAGAAAGACCGGGGCTTGAATGCA 181
Db 121 AGTGGCCAGTTGGCTCATCTGTAAAGATGCCGGAGAAAGACCGGGGCTTGAATGCA 180
Qy 182 GCCAAGTTCAACAAGAGGCGAGAGCCGGCGAGCGGGGTGTGAGCCGGAGAG 241
Db 181 GCCAAGTTCAACAAGAGGCGAGAGCCGGCGAGCGGGGTGTGAGCCGGAGAG 240
Qy 242 ATGAGCGGAGGTGAGCATCTCGGCGAGGTCTGCACCAATGTCTATCAGCTGCAC 301
Db 241 ATGAGCGGAGGTGAGCATCTCGGCGAGGTCTGCACCAATGTCTATCAGCTGCAC 300
Qy 302 GACGCTTATGAAACCGCACCGACGTGTGTCATCTTGAAGTGTGAGAGAG 361
Db 301 GACGCTTATGAAACCGCACCGACGTGTGTCATCTTGAAGTGTGAGAGAG 360
Qy 362 CTCTTGATTTCTGCGCCAGAGAGTCACTAGTGAAGAGAGGCGCACCACTTCATT 421
Db 361 CTCTTGATTTCTGCGCCAGAGAGTCACTAGTGAAGAGAGGCGCACCACTTCATT 420
Qy 422 AAGCAGATCTGATGAGGAGTGAATCACTTCAACAAGAAATTTGATCTGATCTC 481
Db 421 AAGCAGATCTGATGAGGAGTGAATCACTTCAACAAGAAATTTGATCTGATCTC 480
Qy 482 AAGCAGAAACATTAATGTTGTTAGACAAGAAATTTCCATTCACATCAAGCTGATT 541
Db 481 AAGCAGAAACATTAATGTTGTTAGACAAGAAATTTCCATTCACATCAAGCTGATT 540
Qy 542 GACTTTGTCTGCTCAGAAATTAAGATGAGTGAATTTAAGATTTTGGAGC 601
Db 541 GACTTTGTCTGCTCAGAAATTAAGATGAGTGAATTTAAGATTTTGGAGC 600
Qy 602 CCGAAATTTGTTGCTCCAGAAATTTGTAATTCAGAGCCCTGGCTGAGGCTGACATG 661
Db 601 CCGAAATTTGTTGCTCCAGAAATTTGTAATTCAGAGCCCTGGCTGAGGCTGACATG 660
Qy 662 TGGACATAGGCGTCACTACCTCTTAAGTGAAGATCCCTTTCTTGGAGAC 721
Db 661 TGGACATAGGCGTCACTACCTCTTAAGTGAAGATCCCTTTCTTGGAGAC 720
Qy 722 ACGAAGCAGAAACCTGGCAATTCACATCAGAGTTCAGACTTTGATGAGAAATTC 781
Db 721 ACGAAGCAGAAACCTGGCAATTCACATCAGAGTTCAGACTTTGATGAGAAATTC 780
Qy 782 TTCAGCATAGAGAGAGTGGCCAAAGACTTTATTCGAAAGCTTCTGTAAAGAGCC 841
Db 781 TTCAGCATAGAGAGAGTGGCCAAAGACTTTATTCGAAAGCTTCTGTAAAGAGCC 840
Qy 842 CCGAAACGGCTCAATTCAGAGGCTTCAGACACCTCTGATTCACCCGGTGGAGAAC 901
Db 841 CCGAAACGGCTCAATTCAGAGGCTTCAGACACCTCTGATTCACCCGGTGGAGAAC 900
Qy 902 CAGCAAGCATGTTGAGAGGAGGTGTGCTGATCTGAGAACTTCAGAAAGAGTAT 961
Db 901 CAGCAAGCATGTTGAGAGGAGGTGTGCTGATCTGAGAACTTCAGAAAGAGTAT 960

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Qy 962 GTCCGACGCGGTGAGACCTTTCTTCAGACATCGTGTCTCTGTGACACCTCACCCGC 1021
|
|
|
Db 961 GTCCGACGCGGTGAGACCTTTCTTCAGACATCGTGTCTCTGTGACACCTCACCCGC 1020
|
|
|
Qy 1022 TCGCTGATGAAGAGTCCACTGAGCGCCGATGAGACCTGAGAACCTTGAGAGTAC 1081
|
|
|
Db 1021 TCGCTGATGAAGAGTCCACTGAGCGCCGATGAGACCTGAGAACCTTGAGAGTAC 1080
|
|
|
Qy 1082 ACTGAGGAGACATCGCAGAGAGAAACCTCCACCCAGAGAGAGAGACGACCTCC 1141
|
|
|
Db 1081 ACTGAGGAGACATCGCAGAGAGAAACCTCCACCCAGAGAGAGAGACGACCTCC 1140
|
|
|
Qy 1142 TAACTGCGCTGACCTGACGTGCGCCGCAAGGAGTTTGAGGCCAGCGGAGCTCCCTTGTG 1201
|
|
|
Db 1141 TAACTGCGCTGACCTGACGTGCGCCGCAAGGAGTTTGAGGCCAGCGGAGCTCCCTTGTG 1200
|
|
|
Qy 1202 TGGACACTTTTGGACCCAGCTCAGACACGACCCGCGGCTCTGAGACATTTTGGAAAG 1261
|
|
|
Db 1201 TGGACACTTTTGGACCCAGCTCAGACACGACCCGCGGCTCTGAGACATTTTGGAAAG 1260
|
|
|
Qy 1262 AGATGCGCCCAAGAAATTCAGAAAGCTTTCAGGCAACGAGAGACCTGAGAGCTGTG 1321
|
|
|
Db 1261 AGATGCGCCCAAGAAATTCAGAAAGCTTTCAGGCAACGAGAGACCTGAGAGCTGTG 1320
|
|
|
Qy 1322 GCTGTCTTCTGTGAGAGAGGCTCCAGCATTCCTCAAGCTTTAATTTCTCAATAAATGG 1381
|
|
|
Db 1321 GCTGTCTTCTGTGAGAGAGGCTCCAGCATTCCTCAAGCTTTAATTTCTCAATAAATGG 1380
|
|
|
Qy 1382 CTTTCTCTGTCTGTGACATCTCAGAGTCTGGGGTGGAGTGTGACTTGAAGAAAATA 1441
|
|
|
Db 1381 CTTTCTCTGTCTGTGACATCTCAGAGTCTGGGGTGGAGTGTGACTTGAAGAAAATA 1440
|
|
|
Qy 1442 TAAAGACATCTCTCATCATCAGGGGTGAGGTGAGTAAAGGCAAGCTTCTTCACAGGC 1501
|
|
|
Db 1441 TAAAGACATCTCTCATCATCAGGGGTGAGGTGAGTAAAGGCAAGCTTCTTCACAGGC 1500
|
|
|
Qy 1502 TGAGGGGGTTCAGAACCAAGCTGTGCAAAATTAACACAGAGAGACAGAGTCTTCCCAT 1561
|
|
|
Db 1501 TGAGGGGGTTCAGAACCAAGCTGTGCAAAATTAACACAGAGAGACAGAGTCTTCCCAT 1560
|
|
|
Qy 1562 TGGGACAGGGGTGATTGAGAAAGTGAACCTTGGGTGTGAGGAGCAATCTGTGACCTC 1621
|
|
|
Db 1561 TGGGACAGGGGTGATTGAGAAAGTGAACCTTGGGTGTGAGGAGCAATCTGTGACCTC 1620
|
|
|
Qy 1622 CCAGAACCATGGAAGCCAGAGCGTCAAGCTGACCAACCTCAGACCTTCTGAAGCAAGC 1681
|
|
|
Db 1621 CCAGAACCATGGAAGCCAGAGCGTCAAGCTGACCAACCTCAGACCTTCTGAAGCAAGC 1680
|
|
|
Qy 1682 CATTGCTGCGCCGCGCATGTTAAATTTGCTCATTTTAACTTCTGCTTAACTGTA 1741
|
|
|
Db 1681 CATTGCTGCGCCGCGCATGTTAAATTTGCTCATTTTAACTTCTGCTTAACTGTA 1740
|
|
|

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RESULT 6
US-09-652-917-3775
; Sequence 3775, Application US/09652917
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1170-001
; CURRENT APPLICATION NUMBER: US/09/652.917
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151.422
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 3775
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-09-652-917-3775
Query Match          99.24; Score 1728.8; DB 25; Length 2235;
Best Local Similarity 99.64; Pred. No. 0;
Matches 1733; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ACCGCGGAGCTCAGCCCTCCGCGGATTTGATGTTCCAGGCTCAATGAGAGTCCAAAC 61
|
|
|
Db 1 ACCGCGGAGCTCAGCCCTCCGCGGATTTGATGTTCCAGGCTCAATGAGAGTCCAAAC 60
|
|
|
Qy 62 ATGAGACCATTCAGACGACGAGAGTGAAGACCTTTATGACATTCGAGAGAGAGCTGGGG 121
|
|
|
Db 61 ATGAGACCATTCAGACGACGAGAGTGAAGACCTTTATGACATTCGAGAGAGAGCTGGGG 120
|
|
|
Qy 122 AGTGCGCAGTTTGGCATCGTGAAGAAAGTCCGGGAGAAAGACAGCGGGCTTGAATATCA 181
|
|
|
Db 121 AGTGCGCAGTTTGGCATCGTGAAGAAAGTCCGGGAGAAAGACAGCGGGCTTGAATATCA 180
|
|
|
Qy 182 GCCAAGTTTCATCAAGAAAGCCGAGAGCCGCGGAGCCGCGGTGTGAGCCGGAGAGAG 241
|
|
|
Db 181 GCCAAGTTTCATCAAGAAAGCCGAGAGCCGCGGAGCCGCGGTGTGAGCCGGAGAGAG 240
|
|
|
Qy 242 ATCGAGCGGAGGTGAGCATCTCGCGGAGGTGCTGCAACCAATGTCATACGCTGCAC 301
|
|
|
Db 241 ATCGAGCGGAGGTGAGCATCTCGCGGAGGTGCTGCAACCAATGTCATACGCTGCAC 300
|
|
|
Qy 302 GACGCTATGAGAACCCGACCGAGTGTGACATCTCTTGAAGTATGTCGAGAGAGAG 361
|
|
|
Db 301 GACGCTATGAGAACCCGACCGAGTGTGACATCTCTTGAAGTATGTCGAGAGAGAG 360
|
|
|
Qy 362 CTTTCTGATTTCTCGGCCCAAGAGAGTCACTGAGTGAAGAGAGGCCACCAAGCTTCATT 421
|
|
|
Db 361 CTTTCTGATTTCTCGGCCCAAGAGAGTCACTGAGTGAAGAGAGGCCACCAAGCTTCATT 420
|
|
|
Qy 422 AAGCAGATCTCGATGTGGGTGAATCACTCTTCAACAAAGAAATTTGCTCACTTGATTC 481
|
|
|
Db 421 AAGCAGATCTCGATGTGGGTGAATCACTCTTCAACAAAGAAATTTGCTCACTTGATTC 480
|
|
|
Qy 482 AAGCAGAAACATTAATGTTTGTAGCAAGAAATTTCCATTCACATCAATCAACTGATT 541
|
|
|
Db 481 AAGCAGAAACATTAATGTTTGTAGCAAGAAATTTCCATTCACATCAACTGATT 540
|
|
|
Qy 542 GACTTGTGTGCTCAGAAATAGAAATGAGATGTAATTTAAGAAATATTTTGGAGC 601
|
|
|
Db 541 GACTTGTGTGCTCAGAAATAGAAATGAGATGTAATTTAAGAAATATTTTGGAGC 600
|
|
|
Qy 602 CCGGAATTTGTTGCTCCAGAAATTTGTAATGACAGCCCTCGGCTGTGAGGCTGACATG 661
|
|
|
Db 601 CCGGAATTTGTTGCTCCAGAAATTTGTAATGACAGCCCTCGGCTGTGAGGCTGACATG 660
|
|
|
Qy 662 TGGAGCATAGGCGTCACTCACTAATCTCTTAAGTGAAGATCCCTTCTTGGAGAC 721
|
|
|
Db 661 TGGAGCATAGGCGTCACTCACTAATCTCTTAAGTGAAGATCCCTTCTTGGAGAC 720
|
|
|
Qy 722 ACGAAGCAGAAACACTGCGCAATATCATCAGTGAATTCAGACTTTGATGAGAAATTC 781
|
|
|
Db 721 ACGAAGCAGAAACACTGCGCAATATCATCAGTGAATTCAGACTTTGATGAGAAATTC 780
|
|
|
Qy 782 TTCAAGCATAGAGCGAGCTGTGCAAGACCTTTAATGGAAGCTTCTGTGTTAAAGAGCC 841
|
|
|
Db 781 TTCAAGCATAGAGCGAGCTGTGCAAGACCTTTAATGGAAGCTTCTGTGTTAAAGAGCC 840
|
|
|
Qy 842 CCGAAAGCGCTCAATTCAGAAAGGCTCTCAGACACCCCTGTGATCAGCGCGGTGACAC 901
|
|
|
Db 841 CCGAAAGCGCTCAATTCAGAAAGGCTCTCAGACACCCCTGTGATCAGCGCGGTGACAC 900
|
|
|
Qy 902 CAGCAAGCATGAGTGCAGAGCGGAGTGTGTGATCATGAGAACTTCAGGAACAGAT 961
|
|
|
Db 901 CAGCAAGCATGAGTGCAGAGCGGAGTGTGTGATCATGAGAACTTCAGGAACAGAT 960
|
|
|
Qy 962 GTCCGACGCGGTGAGAGCTTCTTCAGACATCGTGTCTCTGTGACACCTCACCCGC 1021
|
|
|
Db 961 GTCCGACGCGGTGAGAGCTTCTTCAGACATCGTGTCTCTGTGACACCTCACCCGC 1020
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QY 1022 TCGCTGATGAAGAGTGCACCTGAGCCGGATGAGGACCTGAGGAATGTGAGAGTGAC 1081
DB 1021 TCGCTGATGAAGAGTGCACCTGAGCCGGATGAGGACCTGAGGAATGTGAGAGTGAC 1080
QY 1082 ACTGAGAGGACATCGCCAGGAGGAAAGCCCTCCACCCAGGAGGAGGAGACAGACCTCC 1141
DB 1081 ACTGAGAGGACATCGCCAGGAGGAAAGCCCTCCACCCAGGAGGAGGAGACAGACCTCC 1140
QY 1142 TAACTGAGCTGACCTGACGTGGCCGCGAGGAGGTTTGGGCCCAAGCGGAGCTCCCTTCTG 1201
DB 1141 TAACTGAGCTGACCTGACGTGGCCGCGAGGAGGTTTGGGCCCAAGCGGAGCTCCCTTCTG 1200
QY 1202 TGCAGACTTTTGGACCCAGCTCAGACCAACACCCGGGCTCTGAGACATTTGCAAGAG 1261
DB 1201 TGCAGACTTTTGGACCCAGCTCAGACCAACACCCGGGCTCTGAGACATTTGCAAGAG 1260
QY 1262 AGATGGGCCCAAGGAATTCAGAAAGCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1321
DB 1261 AGATGGGCCCAAGGAATTCAGAAAGCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
QY 1322 GCTGTCTTGTGAGAGGCTCCAGCATTCCTCAAGCTTTAATTTCTCATTAATAATGAG 1381
DB 1321 GCTGTCTTGTGAGAGGCTCCAGCATTCCTCAAGCTTTAATTTCTCATTAATAATGAG 1380
QY 1382 CTTTCTCTGTCTGCTCCTCCTCAGAGTCTGGGGTGGAGGTGAGACTTGAAGAAACAATA 1441
DB 1381 CTTTCTCTGTCTGCTCCTCCTCAGAGTCTGGGGTGGAGGTGAGACTTGAAGAAACAATA 1440
QY 1442 TAAAGGACATCTCATCATCAGGGGTGAAAGTCAAGTAAAGGAGGAGGAGGAGGAGGAGGAG 1501
DB 1441 TAAAGGACATCTCATCATCAGGGGTGAAAGTCAAGTAAAGGAGGAGGAGGAGGAGGAGGAG 1500
QY 1502 TGAGGGGGTTCAGAACCAAGCTGGCCAAATAACAGAGAGGAGGAGGAGGAGGAGGAGGAG 1561
DB 1501 TGAGGGGGTTCAGAACCAAGCTGGCCAAATAACAGAGAGGAGGAGGAGGAGGAGGAGGAG 1560
QY 1562 TGGGAAACGGGTGATTGAGAAAGTGAACCTTGGGTGAGGAGCAATCTGTGACCTG 1621
DB 1561 TGGGAAACGGGTGATTGAGAAAGTGAACCTTGGGTGAGGAGCAATCTGTGACCTG 1620
QY 1622 CCAGAACCATGAGACCAAGACGTGAGGCTGACCAACCTTCCTGAGAGGAGC 1681
DB 1621 CCAGAACCATGAGACCAAGACGTGAGGCTGACCAACCTTCCTGAGAGGAGC 1680
QY 1682 CATTCGTGGCCGCGCATGTGTAATTTGCTCATTTTAACTTCTGCTTAACTGTA 1741
DB 1681 CATTCGTGGCCGCGCATGTGTAATTTGCTCATTTTAACTTCTGCTTAACTGTA 1740

RESULT 7
US-09-698-010-12235
Sequence 12235, Application US/09698010
GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.2029-001
CURRENT APPLICATION NUMBER: US/09/698,010
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,358
PRIOR FILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 15684
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12235
LENGTH: 2235
TYPE: DNA
ORGANISM: Homo sapiens
US-09-698-010-12235

Query Match 99.2%; Score 1728.8; DB 27; Length 2235;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1733; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 ACCGCGAGCTCAGCTCCCGGATTTGATTTGACGGCTTCATAGAGGAGTCCAAAC 61
DB 1 ACCGCGAGCTCAGCTCCCGGATTTGATTTGACGGCTTCATAGAGGAGTCCAAAC 60
QY 62 ATGAGCATTTCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121
DB 61 ATGAGCATTTCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 122 AGTGGCAGTTTGCATCTGTAAGAGTGCCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
DB 121 AGTGGCAGTTTGCATCTGTAAGAGTGCCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 182 GCCAAGTTGATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
DB 181 GCCAAGTTGATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 242 ATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 301
DB 241 ATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 302 GACGTATGAGAACCGACCGAGCTGTGACATCTTGAAGTGTCTGAGAGAG 361
DB 301 GACGTATGAGAACCGACCGAGCTGTGACATCTTGAAGTGTCTGAGAGAG 360
QY 362 CTCTTGATTTCTGAGCCAGAGGAGTCACTGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAG 421
DB 361 CTCTTGATTTCTGAGCCAGAGGAGTCACTGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 422 AAGCAGATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 481
DB 421 AAGCAGATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 482 AAGCAGAAATCTTATGTTAGCAAGAAATTTCCATTCCACATCAAGCTGAT 541
DB 481 AAGCAGAAATCTTATGTTAGCAAGAAATTTCCATTCCACATCAAGCTGAT 540
QY 542 GACTTGGTCTGCTCAGAAATGTAAGATGAGGTTGAATTTAAGAAATTTTGGAGG 601
DB 541 GACTTGGTCTGCTCAGAAATGTAAGATGAGGTTGAATTTAAGAAATTTTGGAGG 600
QY 602 CCGGAATTTGTTGCTCCAGAAATTTGTAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 661
DB 601 CCGGAATTTGTTGCTCCAGAAATTTGTAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 662 TGGACATAGGCGTATCACTACATCTTTAAGTGAAGCAATCCCTTCTGGGAGGAG 721
DB 661 TGGACATAGGCGTATCACTACATCTTTAAGTGAAGCAATCCCTTCTGGGAGGAG 720
QY 722 ACGAAGCAGAAACCTGGCAAAATTCATCATGATGAGTTACGACTTGTAGAGAAATTC 781
DB 721 ACGAAGCAGAAACCTGGCAAAATTCATCATGATGAGTTACGACTTGTAGAGAAATTC 780
QY 782 TTCAGCATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 841
DB 781 TTCAGCATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 842 CGGAACGCTCAATCCAAAGGCTCTCAGACACCCCTGATCAACGCGGTGAGCAAC 901
DB 841 CGGAACGCTCAATCCAAAGGCTCTCAGACACCCCTGATCAACGCGGTGAGCAAC 900
QY 902 CAGCAAGCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 961
DB 901 CAGCAAGCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 962 GTCCGAGGCGGTGAGAGCTTTCTTACAGCACTGCTGCTGCAACCACTGAGAGTGC 1021
DB 961 GTCCGAGGCGGTGAGAGCTTTCTTACAGCACTGCTGCTGCAACCACTGAGAGTGC 1020
QY 1022 TCGCTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1081
DB 1021 TCGCTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080

QY 1082 ACTGAGAGGACATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGACGACCTCC 1141
 Db 1081 ACTGAGAGGACATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGACGACCTCC 1140
 QY 1142 TAACTGCGCTTACCTGACGAGTCCCGCCAGAGAGGTTTGGGCCAGCGGGGCTCCCTTCTG 1201
 Db 1141 TAACTGCGCTTACCTGACGAGTCCCGCCAGAGAGGTTTGGGCCAGCGGGGCTCCCTTCTG 1200
 QY 1202 TGACAGACTTTTGGACCCAGCTCAGACACGACCCCGGGGCTCTGAGACCTTTGCAAGAG 1261
 Db 1201 TGACAGACTTTTGGACCCAGCTCAGACACGACCCCGGGGCTCTGAGACCTTTGCAAGAG 1260
 QY 1262 AGATGGGCCCAAGAAATTCAAGAGAGCTTGGACGACGACGACGACGACGACGACGACGACG 1321
 Db 1261 AGATGGGCCCAAGAAATTCAAGAGAGCTTGGACGACGACGACGACGACGACGACGACGACG 1320
 QY 1322 GCTGCTCTTCTGAGAGAGGCTCCAGCAATTCGCAAGCTTTAATTCTTCATTAATAATGGG 1381
 Db 1321 GCTGCTCTTCTGAGAGAGGCTCCAGCAATTCGCAAGCTTTAATTCTTCATTAATAATGGG 1380
 QY 1382 CTTCCTCTCTGCTGACATCTCAGAGTCTGGGGTGGAGTGGAGCTTGAAGAAAACAATA 1441
 Db 1381 CTTCCTCTCTGCTGACATCTCAGAGTCTGGGGTGGAGTGGAGCTTGAAGAAAACAATA 1440
 QY 1442 TAAAGACATCTCATCATCAAGGGGTGAAGGTGAGTAAGGACGCTTCTTCACAGGC 1501
 Db 1441 TAAAGACATCTCATCATCAAGGGGTGAAGGTGAGTAAGGACGCTTCTTCACAGGC 1500
 QY 1502 TGAGGGGGTTCAGAACAGGCTGGCCAAAATAATACACAGAGAGACAGAGTCTCCCAT 1561
 Db 1501 TGAGGGGGTTCAGAACAGGCTGGCCAAAATAATACACAGAGAGACAGAGTCTCCCAT 1560
 QY 1562 TGGGAACAGGGTGAATTGGAAGAAAGTGAACCTTGGGTGAGAGGACCAATCCTTGACCTC 1621
 Db 1561 TGGGAACAGGGTGAATTGGAAGAAAGTGAACCTTGGGTGAGAGGACCAATCCTTGACCTC 1620
 QY 1622 CCAGAACCATGGAAGCCAGAGGCTGACGACGACGACGACGACGACGACGACGACGACG 1681
 Db 1621 CCAGAACCATGGAAGCCAGAGGCTGACGACGACGACGACGACGACGACGACGACGACG 1680
 QY 1682 CATGCTGGCCCGCCAGTGTGAATTTTGTCTAATTTTAACTTGTGTTAACTCTGA 1741
 Db 1681 CATGCTGGCCCGCCAGTGTGAATTTTGTCTAATTTTAACTTGTGTTAACTCTCTGA 1740

RESULT 8
 US-09-698-013-6041
 ; Sequence 6041, Application US/09698013
 ; GENERAL INFORMATION:
 ; APPLICANT: Gearing, David P.
 ; APPLICANT: Comrack, Christopher
 ; APPLICANT: Kingsbury, Gillian A.
 ; APPLICANT: Holzman, Douglas A.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 ; FILE REFERENCE: 1600, 2013-001
 ; CURRENT APPLICATION NUMBER: US/09/698, 013
 ; CURRENT FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: 60/162,360
 ; NUMBER OF SEQ ID NOS: 7935
 ; SOFTWARE: FaastSeq for Windows Version 4.0
 ; SEQ ID NO 6041
 ; LENGTH: 2235
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-698-013-6041

Query Match 99.2%; Score 1728.8; DB 27; Length 2235;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1733; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 ACCGCGAGCTCAGCCTCCCGCGATTGATGTTCCAGGCTCAATGAGAGTCCAAAC 61
 Db 1 ACCGCGAGCTCAGCCTCCCGCGATTGATGTTCCAGGCTCAATGAGAGTCCAAAC 60
 QY 62 ATGAGCCATTCAAGACAGACAGAGAGTGAAGACTTTTATGACATTCGAGAGAGAGTGGG 121
 Db 61 ATGAGCCATTCAAGACAGACAGAGAGTGAAGACTTTTATGACATTCGAGAGAGAGTGGG 120
 QY 122 AGTGCCAGTTTGGCATGTGAAGAGTCCGGGAGAAAGACAGGGGCTTGAATATCA 181
 Db 121 AGTGCCAGTTTGGCATGTGAAGAGTCCGGGAGAAAGACAGGGGCTTGAATATCA 180
 QY 182 GCCAAGTTCAATCAAGAGCGGACAGCCGGGCGAGCGCGGTGTGAGCGCGGAGAG 241
 Db 181 GCCAAGTTCAATCAAGAGCGGACAGCCGGGCGAGCGCGGTGTGAGCGCGGAGAG 240
 QY 242 ATCGAGCGGAGGTGAGATCTCTGCGGAGGTGCTGCACCAATGTATCATCGCTGCAC 301
 Db 241 ATCGAGCGGAGGTGAGATCTCTGCGGAGGTGCTGCACCAATGTATCATCGCTGCAC 300
 QY 302 GACGCTATGAGAACCGGACCGAGGTGGTGCATCTCTTGAAGTCTGAGAGAGAG 361
 Db 301 GACGCTATGAGAACCGGACCGAGGTGGTGCATCTCTTGAAGTCTGAGAGAGAG 360
 QY 362 CTCTTCGATTTCTGCGCCAGAGAGAGTCACTGAGTGAAGAGAGGCGCACGCTTCATT 421
 Db 361 CTCTTCGATTTCTGCGCCAGAGAGAGTCACTGAGTGAAGAGAGGCGCACGCTTCATT 420
 QY 422 AAGCAGATCTGAGATGGGGTGAATCACTTCAACAAAGAAATTTGCTCACTTTGATTC 481
 Db 421 AAGCAGATCTGAGATGGGGTGAATCACTTCAACAAAGAAATTTGCTCACTTTGATTC 480
 QY 482 AAGCAGAAACATTAATGTTTGAACAAGATTTCCATTCACATCAATCAAGCTGATT 541
 Db 481 AAGCAGAAACATTAATGTTTGAACAAGATTTCCATTCACATCAATCAAGCTGATT 540
 QY 542 GACTTTGCTGCTGCTCAAGAAATGAAGATGAGTTGATTTAAGAAATTTTGGAGCG 601
 Db 541 GACTTTGCTGCTGCTCAAGAAATGAAGATGAGTTGATTTAAGAAATTTTGGAGCG 600
 QY 602 CCGAATTTGTTGCTCCAGAAATTTGTAATCAAGAGCCCTGGGTCTGAGAGCTGACATG 661
 Db 601 CCGAATTTGTTGCTCCAGAAATTTGTAATCAAGAGCCCTGGGTCTGAGAGCTGACATG 660
 QY 662 TGGAGCATAGGCGTCAATCACTTCAATCCTTAAGTGAAGATCCCTTTCTGGAGAC 721
 Db 661 TGGAGCATAGGCGTCAATCACTTCAATCCTTAAGTGAAGATCCCTTTCTGGAGAC 720
 QY 722 ACGAAGCAGAAACATGCGCAATATATCATCATGATGATTCAGACTTTGATGAGAAATTC 781
 Db 721 ACGAAGCAGAAACATGCGCAATATATCATCATGATGATTCAGACTTTGATGAGAAATTC 780
 QY 782 TTGAGCCATAGAGCGAGCTGGCCAGAGACTTTAATGGAAGCTTGTGTTAAAGAGAC 841
 Db 781 TTGAGCCATAGAGCGAGCTGGCCAGAGACTTTAATGGAAGCTTGTGTTAAAGAGAC 840
 QY 842 CGGAAACGCTCAATTCAGAGAGCTTCTGACACACCCCTTGATTCAGCGCGGTGACAAAC 901
 Db 841 CGGAAACGCTCAATTCAGAGAGCTTCTGACACACCCCTTGATTCAGCGCGGTGACAAAC 900
 QY 902 CAGCAAGCATGCTGCGAGCGGAGTCTGTGTCATCTGAGAACTTCAGAGACAGATAT 961
 Db 901 CAGCAAGCATGCTGCGAGCGGAGTCTGTGTCATCTGAGAACTTCAGAGACAGATAT 960
 QY 962 GTCCGAGCGGTGAAAGCTTCTTCAAGATCGTGTCTCTGTCACCACTTCAAGAGAGAT 1021
 Db 961 GTCCGAGCGGTGAAAGCTTCTTCAAGATCGTGTCTCTGTCACCACTTCAAGAGAGAT 1020
 QY 1022 TCGCTGATGAAGAGGTGACATCTGAGGCGGATGAGAGCTTGAAGAACTGTAAGATGAC 1081
 Db 1021 TCGCTGATGAAGAGGTGACATCTGAGGCGGATGAGAGCTTGAAGAACTGTAAGATGAC 1080
 QY 1082 ACTGAGAGGACATCGCCAGAGAGAAAGCCTCCACCCAGAGAGAGAGACGACCTCC 1141

| | | | |
|----|------|---|------|
| Db | 1081 | ACTGAGAGGACATCCGACAGAGGAAAGCCCTTCACCCACGAGAGGAGAGGACGACCTCC | 1140 |
| Qy | 1142 | TAACTGAGCTGACCTGTGACGTGGCCGACAGAGGTTTGGGCCCAAGCGGGGCTCCCTTCTG | 1201 |
| Db | 1141 | TAACTGGCTGACCTGTGACGTGGCCGACAGAGGTTTGGGCCCAAGCGGGGCTCCCTTCTG | 1200 |
| Qy | 1202 | TGCAGACTTTTGGACCCAGCTTGAAGACCAAGCAACCGGGGGTCTGAGCACTTTGCAAG | 1261 |
| Db | 1201 | TGCAGACTTTTGGACCCAGCTTGAAGACCAAGCAACCGGGGGTCTGAGCACTTTGCAAG | 1260 |
| Qy | 1262 | AGATGGGCCCAAGAAATTCAGAAAGCTTGACGAGCAAGCCAGACCTCTGGGAACTGTG | 1321 |
| Db | 1261 | AGATGGGCCCAAGAAATTCAGAAAGCTTGACGAGCAAGCCAGACCTCTGGGAACTGTG | 1320 |
| Qy | 1322 | GCTGCTCTTCTGTGAGAGGAGCTCCAGAGTTCCCAAAGCTTTAATCTCCATPAAATGGG | 1381 |
| Db | 1321 | GCTGCTCTTCTGTGAGAGGAGCTCCAGAGTTCCCAAAGCTTTAATCTCCATPAAATGGG | 1380 |
| Qy | 1382 | CTTTCTCTGTCTGTGCATCTCAGAGTCTGGGGTGGGAGTGTGGACTTGAAGAAACAATA | 1441 |
| Db | 1381 | CTTTCTCTGTCTGTGCATCTCAGAGTCTGGGGTGGGAGTGTGGACTTGAAGAAACAATA | 1441 |
| Qy | 1442 | TAAAGACATCTCTATCATCAACGGGGTGAAGTCAAGTAAGCAGCTTCTTCAAGGC | 1501 |
| Db | 1441 | TAAAGACATCTCTATCATCAACGGGGTGAAGTCAAGTAAGCAGCTTCTTCAAGGC | 1500 |
| Qy | 1502 | TGAGGGGTTTCAGAACCAAGCTGGCCAAAATTAACAACAGAGACAGATCTCCCCAT | 1561 |
| Db | 1501 | TGAGGGGTTTCAGAACCAAGCTGGCCAAAATTAACAACAGAGACAGATCTCCCCAT | 1560 |
| Qy | 1562 | TGGGAACAGGGAGATTGAGAAAGTGAACCTTTGGGTGTGAAGGACCAATCTGTGACTC | 1621 |
| Db | 1561 | TGGGAACAGGGAGATTGAGAAAGTGAACCTTTGGGTGTGAAGGACCAATCTGTGACTC | 1620 |
| Qy | 1622 | CCAGAACCATGAAAGCCAGAGCTCAGGCTGACCAACCTCAGACCTTGAAGCAGCC | 1681 |
| Db | 1621 | CCAGAACCATGAAAGCCAGAGCTCAGGCTGACCAACCTTGAAGCAGCC | 1680 |
| Qy | 1682 | CATTGCTGGCCGACATGTGTAAATTTGCTCATTTTAACTTGTGTTTAACTGTA | 1741 |
| Db | 1681 | CATTGCTGGCCGACATGTGTAAATTTGCTCATTTTAACTTGTGTTTAACTGTA | 1740 |

| | | | |
|----|------|---|------|
| Db | 12 | GACCGCGGACGCTCAGCGCTCCGCGCATTTGATGTTCCAGGCGCTCAATGAGGAGTCCAAA | 71 |
| Qy | 61 | CATGGAGCATTTCAAGCAGAGAAAGGTGAGNACITTTATGACATCGAGAGAGACTGGG | 120 |
| Db | 72 | CATGAGGCACTTCAAGCAGCAGAAAGGTGAGGACTTTTATGACATCGGAGAGAGACTGGG | 131 |
| Qy | 121 | GAGTGGCCAGTTGGCCATCGTGAAAGAGTCCCGGAGAAAGAGACGAGGGCTTGAGTATGC | 180 |
| Db | 132 | GAGTGGCCAGTTGGCCATCGTGAAAGAGTCCCGGAGAAAGAGACGAGGGCTTGAGTATGC | 191 |
| Qy | 181 | AACCAAGTTCATCAAGAAAGCGGCGAGACCGGGGAGGCGGCGGCTGTGAGCCGGAGGA | 240 |
| Db | 192 | AACCAAGTTCATCAAGAAAGCGGCGAGACCGGGGAGGCGGCGGCTGTGAGCCGGAGGA | 251 |
| Qy | 241 | GATCGAGCGGAGGTGAGCATCTGCGGCAAGTGTCTGCACCAAAATGTACACGGCTGCA | 300 |
| Db | 252 | GATCGAGCGGAGGTGAGCATCTGCGGCAAGTGTCTGCACCAAAATGTACACGGCTGCA | 311 |
| Qy | 301 | CGAGCTCTATGAGAACCCGACCGAGCTGTGTGACATCTTGAGCTAGTGTCTGAGAGAA | 360 |
| Db | 312 | CGAGCTCTATGAGAACCCGACCGAGTGTGTCTATCTTGAGCTAGTGTCTGAGAGAA | 371 |
| Qy | 361 | GCATCTCGATTTCTGTGCGCCAGAAAGAGTCTAATGATGAGAGAGGCGCACAGCTTCAT | 420 |
| Db | 372 | GCATCTCGATTTCTGTGCGCCAGAAAGAGTCTAATGATGAGAGAGGCGCACAGCTTCAT | 431 |
| Qy | 421 | TAAAGAGATCTGATGGGGTAACTACCTTTCACAAAGAAAATTTCTCACTTTGATCT | 480 |
| Db | 432 | TAAAGAGATCTGAGTGGGGTAACTACCTTTCACAAAGAAAATTTCTCACTTTGATCT | 491 |
| Qy | 481 | CAAGCCAGAAAACATTATGTGTGTAGACAGAAATTTCCATTCACATCAAGCTGAT | 540 |
| Db | 492 | CAAGCCAGAAAACATTATGTGTGTAGACAGAAATTTCCATTCACATCAAGCTGAT | 551 |
| Qy | 541 | TGACTTTTGATCTGCGCTTCAGAAATGAGATGGAATTTTAAGAAATTTTGTGGAC | 600 |
| Db | 552 | TGACTTTTGATCTGCGCTTCAGAAATGAGATGGAATTTTAAGAAATTTTGTGGAC | 611 |
| Qy | 601 | GCCGGAAATTTGTGTCTCAGAAATGTGAATCTACGAGCCCTGTGGTCTGAGGCTGACAT | 660 |
| Db | 612 | GCCGGAAATTTGTGTCTCAGAAATGTGAATCTACGAGCCCTGTGGTCTGAGGCTGACAT | 671 |
| Qy | 661 | GTGAGCATAGGCGCTCATCACTTACATCTCTTAAGTGAACATCCCTTCTCGGGAGA | 720 |
| Db | 672 | GTGAGCATAGGCGCTCATCACTTACATCTCTTAAGTGAACATCCCTTCTCGGGAGA | 731 |
| Qy | 721 | CACGAGCAGAAACATCTGGCAAAATATCAATGAGAGTACGATTTGATGAGAAAT | 780 |
| Db | 732 | CACGAGCAGAAACATCTGGCAAAATATCAATGAGAGTACGATTTGATGAGAAAT | 791 |
| Qy | 781 | CTTGAGCATTCAGAGCAGAGCTGGCCAAAGACATTTATTCGAGACTTCTGTAAAGAGC | 840 |
| Db | 792 | CTTGAGCATTCAGAGCAGAGCTGGCCAAAGACATTTATTCGAGACTTCTGTAAAGAGC | 851 |
| Qy | 841 | CCGAGAAACGGCTCACATCCAAAGGCTCTCAAGACCCCTGGATCACGCCGCTGAGCAA | 900 |
| Db | 852 | CCGAGAAACGGCTCACATCCAAAGGCTCTCAAGACCCCTGGATCACGCCGCTGAGCAA | 911 |
| Qy | 901 | CCAGCAAGCAGTGTGCAACGAGAGCTGTGTGCAATCTGAGAACTTCAGAAAGCAT | 960 |
| Db | 912 | CCAGCAAGCAGTGTGCAACGAGAGCTGTGTGCAATCTGAGAACTTCAGAAAGCAT | 971 |
| Qy | 961 | TGTCCGACGCGGTGAGAGCTTCTCTTCAGCATGTGTCTCTGTGCAACCAACCTCACCCG | 1020 |
| Db | 972 | TGTCCGACGCGGTGAGAGCTTCTCTTCAGCATGTGTCTCTGTGCAACCAACCTCACCCG | 1031 |
| Qy | 1021 | CTGCTGATGAAAGAGTGCACCTGAGGCGGATGAGAGACT---GAGNAACTGTGAGA | 1076 |
| Db | 1032 | CTGCTGATGAAAGAGTGCACCTGAGGCGGATGAGAGACT---GAGNAACTGTGAGA | 1091 |
| Qy | 1077 | GTACACCTGAGAGCATCTGCGCAGAGAGAAAGCCCTTCACCTCACGAGAGAGAGAGCA | 1136 |

| | | | | |
|----------------------------|-------|---------------------|-----------|--------------|
| Query Match | 59.8% | Score 1042.2; | DB 29; | Length 1864; |
| Best Local Similarity | 99.2% | Pred. No. 2.8e-245; | | |
| Matches 1047; Conservative | 0; | Mismatches 8; | Indels 0; | Gaps 0; |

| | | | |
|----|------|---|------|
| Qy | 687 | TCCTCTTAAGGGAGGACATCCCTTCTCTGGAGACACGAAGCAGGAAAACATGGCAAAAT | 746 |
| Db | 300 | TCAGCTTAAGTGGAGCATCCCTTCTCTGGAGACAGAAAGAGAAAACATGGCAAAAT | 359 |
| Qy | 747 | TCACATCAGTGAAGTATGCACTTTGATGAGGAATTTCTTCAGCATATGAGCGAGCTGGCCA | 806 |
| Db | 360 | TCACAGCAGTGAAGTATGCACTTTGATGAGGAATTTCTTCAGCATATGAGCGAGCTGGCCA | 419 |
| Qy | 807 | AGGACTTTAATTCGGAAGCTTCTGTGTTAAAGAGACCGGAAACGGCTCACAATCCAAAGAG | 866 |
| Db | 420 | AGGACTTTAATTCGGAAGCTTCTGTGTTAAAGAGACCGGAAACGGCTCACAATCCAAAGAG | 479 |
| Qy | 867 | CTTCACACACCCCTGGATGACCCCGGTGACACACAGCAAGCAATGGTGGCAGCGGAGT | 926 |
| Db | 480 | CTTCACACACCCCTGGATGACCCCGGTGACACACAGCAAGCAATGGTGGCAGCGGAGT | 539 |
| Qy | 927 | CTGTGTCTCAATCTTGAGAGACCTTCAGAGAAAGATGTCCGACAGCGGTGGAAGCTTCTCT | 986 |
| Db | 540 | CTGTGTCTCAATCTTGAGAGACCTTCAGAGAAAGATGTCCGACAGCGGTGGAAGCTTCTCT | 599 |
| Qy | 987 | TCAGCATCGTGTCCCTGTGTGCAACCACTCAACCCGCTCGCTGATGAAGAAAGTGCACCTGA | 1044 |
| Db | 600 | TCAGCATCGTGTCCCTGTGTGCAACCACTCAACCCGCTCGCTGATGAAGAAAGTGCACCTGA | 659 |
| Qy | 1047 | GGCCGGATGAGAGACTTGAGAGACCTTGAGAGTGAACACTGAGAGAGACATCCGACAGAGGA | 1100 |
| Db | 660 | GGCCGGATGAGAGACTTGAGAGACCTTGAGAGTGAACACTGAGAGAGACATCCGACAGAGGA | 719 |
| Qy | 1107 | AAGCCCTCCACCCACGGAGAGAGAGACGACCTCCPACTGGCGTGAACCTGGACGTGGCCG | 1166 |
| Db | 720 | AAGCCCTCCACCCACGGAGAGAGAGACGACCTCCPACTGGCGTGAACCTGGACGTGGCCG | 779 |
| Qy | 1167 | CCAGGAGAGTGTGGGCCACAGCGGGGCTCCCTTCTGTGACAGCTTTTGGACCCGACCTCAC | 1222 |
| Db | 780 | CCAGGAGAGTGTGGGCCACAGCGGGGCTCCCTTCTGTGACAGCTTTTGGACCCGACCTCAC | 839 |
| Qy | 1227 | ACCAACGACCCGGGGGCTCTGAGACACTTTGCAGAGAGATGGGCCCAAGAAATTCAGAGGA | 1288 |
| Db | 840 | ACCAACGACCCGGGGGCTCTGAGACACTTTGCAGAGAGATGGGCCCAAGAAATTCAGAGGA | 899 |
| Qy | 1287 | GCTTGACGGGCAAGCAGAGAACCTCTGGAGCTGTGGCTGTCTTCTGTGAGAGAGGCTCA | 1344 |
| Db | 900 | GCTTGACGGGCAAGCAGAGAACCTCTGGAGCTGTGGCTGTCTTCTGTGAGAGAGGCTCA | 959 |
| Qy | 1347 | GCATTTCCCAAAGCTCTTAATTTCTCCATPAAAATGGGCTTTCTCTGTCTCCATCTCCAGA | 1400 |
| Db | 960 | GCATTTCCCAAAGCTCTTAATTTCTCCATPAAAATGGGCTTTCTCTGTCTCCATCTCCAGA | 1011 |
| Qy | 1407 | GTCGTGGGGTGGAGTGTGACTTAGGAAAACAATATPAAGACATCTCATCATCAACGGG | 1466 |
| Db | 1020 | GTCGTGGGGTGGAGTGTGACTTAGGAAAACAATATPAAGACATCTCATCATCAACGGG | 1076 |
| Qy | 1467 | GTCGAAGCTCAGAGTAAAGGCAAGCTTTCTTCACAGGCTGAGGGGGTTAGAAACCAAGCTGGC | 1522 |
| Db | 1080 | GTCGAAGCTCAGAGTAAAGGCAAGCTTTCTTCACAGGCTGAGGGGGTTAGAAACCAAGCTGGC | 1133 |
| Qy | 1527 | CAAAATTTAACAACAGAGAGACAGAGTCTCCCACTTGGGAAACAGGGTGAATTGAGGAAAT | 1588 |
| Db | 1140 | CAAAATTTAACAACAGAGAGACAGAGTCTCCCACTTGGGAAACAGGGTGAATTGAGGAAAT | 1199 |
| Qy | 1587 | GAACTTTGGGTGTGAGGAGCAATTCCTGTGACCTCCACAGAACCATGAGAACCAAGGACGTC | 1644 |
| Db | 1200 | GAACTTTGGGTGTGAGGAGCAATTCCTGTGACCTCCACAGAACCATGAGAACCAAGGACGTC | 1255 |
| Qy | 1647 | AGGCTGACCAACACTCAGACTTCTGAGACAGCCATTGCTGGCCCGCATGTTGTAAT | 1700 |
| Db | 1260 | AGGCTGACCAACACTCAGACTTCTGAGACAGCCATTGCTGGCCCGCATGTTGTAAT | 1311 |
| Qy | 1707 | TTTGCTCATTTTTATTAACCTTCGGTTAACCGGA | 1741 |
| Db | 1320 | TTTGCTCATTTTTATTAACCTTCGGTTAACCGGA | 1354 |

RESULT 11
US-60-360-207-3361
; Sequence 3361, Application us/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: C0001321
; CURRENT APPLICATION NUMBER: US/60/360,207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 3361
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-3361

Query Match 59.3%; Score 1032.4; DB 80; Length 1732;
Best Local Similarity 83.8%; Pred. No. 7e-243;
Matches 1263; Conservative 0; Mismatches 186; Indels 59; Gaps 6;

QY 8 GCAGCTCAGCCCTCCCGCATTTGATGTTCCAGGCTCATAGAGATCCAAATGAG 67
DB 91 GCAGCCGAGCTTTCCCGATTTGATGTTCCAGGCTCATAGAGATCCAAATGAG 150
QY 68 CCATTCAAGCAGCAGAGAGTGAAGACTTTTATGACATGAGAGAGCTGGGAGTGGC 127
DB 151 ACCTTCAAACAGCAGAGAGTGAAGACTTTTATGACATGAGAGAGCTGGGAGTGGC 210
QY 128 CAGTTTCCATTCGTGAAGAGTCCCGGAGAGAGCAGCGGCTTGAATGAGCAG 187
DB 211 CAGTTTCCATTCGTGAAGAGTCCCGGAGAGAGCAGCGGCTTGAATGAGCAG 270
QY 188 TTCTCAAGAGCGCAGAGCCCGGCGAGCCGCGGTGTGAGCCCGGAGAGATCGAG 247
DB 271 TTCTCAAGAGCGCAGAGCCCGGCGAGCCGCGGTGTGAGCCCGGAGAGATCGAG 330
QY 248 CGGAGGTGAGATCTCTGCGGAGAGTGTGACCAATGTCATCGCTGAGAGAGTGC 307
DB 331 CGGAGGTGAGATCTCTGCGGAGAGTGTGACCAATGTCATCGCTGAGAGAGTGC 390
QY 308 TATAGAGAGCGCAGAGCTGTGACATCTTGTGAGTGTGTGAGAGAGAGTCTTTC 367
DB 391 TATAGAGAGCGCAGAGCTGTGACATCTTGTGAGTGTGTGAGAGAGAGTCTTTC 450
QY 368 GATTTCCTGCGCCAGAGAGTCACTGAGTGAAGAGAGAGCCACACCTTCATTAAAGCAG 427
DB 451 GATTTCCTGCGCCAGAGAGTCACTGAGTGAAGAGAGAGCCACACCTTCATTAAAGCAG 510
QY 428 ATCTCGATGGGGTGAATCTACCTTCAACAAGAAATTTGCTCACTTGAATCTCAAGCCA 487
DB 511 ATCTCGATGGGGTGAATCTACCTTCAACAAGAAATTTGCTCACTTGAATCTCAAGCCA 570
QY 488 GAAACATTATGTTGTGAACAAGAAATTTCCATTCCACATCACTGATTTGATTT 547
DB 571 GAAACATTATGTTGTGAACAAGAAATTTCCATTCCACATCACTGATTTGATTT 630
QY 548 GGTCTGCGCTCAGAAATGAAGATGAAGTGAATTTAAATTTTGGAGCCCGGAA 607
DB 631 GGTCTGCGCTCAGAAATGAAGATGAAGTGAATTTAAATTTTGGAGCCCGGAA 690
QY 608 TTTGTGCTCCAGAAATTTGAAGTGAAGAGCCCTGGGTCTGAGAGCTGACATGTGAGC 667
DB 691 TTTGTGCTCCAGAAATTTGAAGTGAAGAGCCCTGGGTCTGAGAGCTGACATGTGAGC 746
QY 668 ATAGGCGTCATCACTTACCTTTAAGTGAAGATCCCTTCTCTGGAGAGACAGAG 727
DB 747 -----TCTAAGTGAAGCTTCCCTTCTCTGGAGAGACAGAG 783
QY 728 CAGAGAAACCTGGCAATATCATCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 787
DB 784 CAGAGAAACCTGGCAATATCATCATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 843
QY 788 CATACGAGCAGCTGGCCAAAGACTTTATTCGAGAGCTTCTGTATTAAGAGCCGAGAA 847

DB 844 CAGAGAGCAGAGCTGGCCAAAGACTTCAATTCGAGAGCTTCTGTGAAGAGACCCGAGAA 903
QY 848 CGGCTCACAATCCAAAGAGCTTCTGACACACCCCTGATATACCGCGGTGACCAACAGCAA 907
DB 904 CGGCTTACATCCAAAGAGCTTCTGACATCCCTGATATACCGCGGTGACCAACAGCAA 963
QY 908 GCCATGTGGCCAGCGGAGTCTGTGATCAATCTGAGAGACTTCAGAGACAGTATGTCCG 967
DB 964 GCTATGTGACGAGAGAGTCCGTGTCACTGAGAAATTTAAGAGACATATGTCCG 1023
QY 968 AGCGGTGAGACTTCTTCCCTTCCAGATCTGTCTGTCGAAACCACTTCCGCTGCTG 1027
DB 1024 AGCGGTGAGACTTCTTCCCTTCCAGATCTGTCTGTCGAAACCACTTCCGCTGCTG 1083
QY 1028 ATGAGAGAGTCACTTGAAGCGGAGATGAGAGCTGAGAACTGTGAGTGAAGTGAAG 1087
DB 1084 ATGAGAGAGTCACTTGAAGCGGAGACAGAGACTGAGAGACTGAGAGAGTGAAGTGAAG 1143
QY 1088 GAGAGATGCGCAGAGAGAAAGCCCTCCACCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1147
DB 1144 GAGAGATGCGCAGAGAGAAAGCCCTTCACTCCGAGAGAGAGAGAGAGAGAGAGAGAG 1203
QY 1148 GCCTGACCTGAGTGGCCCGCAGAGAGTGTGGGCGCCAGCGGAGCTCCCTTCTGTGAGA 1207
DB 1204 GCCAGCTTGCAGTGTGCTGCGAGAGAGTCCAG---TTCTGCGGCTTGTGTGAGAG 1260
QY 1208 CTTTGGAGCCAGCTGAGCAGCAGCAGCCGAGG-----TCTGAGCACTTTGAGAG 1259
DB 1261 CTCCCGAGCTTGTGTGAGTCACTGAGATCCAGACATTTCTGTGTTCTGAGACACTTTGAG 1320
QY 1260 AGAGATGGGCCAAAGATTCAGAGAGCTTGCAGAGCAGAGAGAGAGAGAGAGAGAGAG 1319
DB 1321 AGAGAGATGCTGAGAGAGTCAAGAACTTT-----CCGAGAGCCCTGGAGAGTGG 1368
QY 1320 TGGCTGTCTTGTGAGAGAGGCTCCAGATTCCTCAAGAGCTTTAATTCATTAATAG 1379
DB 1369 TGGCTGTCTTGTGAGAGAGGCTCCAGATTCCTCAAGAGCTTTAATTCATTAATAG 1428
QY 1380 GGTCTTCTGTGTGCTGCTGATCTGAGAGTGTGGGTGGAGTGTGAGCTTAAGAGAAACAA 1439
DB 1429 GGTCTTCTGTGTGCTGCTGATCTGAGAGTGTGGGTGGAGTGTGAGCTTAAGAGAAATGGA 1487
QY 1440 TATTAAGAG-----CATCTCATCATCAGCGGCTGAAGTGTGAGTGAAGCAGCTTT 1491
DB 1488 TCTCAAGAGATCTTTTATTTTAAACAGAGTTAAAGTGAAGTGAAGCAGCTTT 1547
QY 1492 CTTACAG 1499
DB 1548 CTTACAG 1555

RESULT 12
US-09-649-163-7647
; Sequence 7647, Application us/09649163
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Galvin, Katherine A.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Kingsbury, Gillian A.
; APPLICANT: Welch, Nadine S.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Williamson, Mark
; APPLICANT: Richardson, Jennifer
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Frazer, Christopher C.
; APPLICANT: Villevall, Jean-Luc M.G.
; APPLICANT: Goodheart, Andrew D.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; APPLICANT: Busfield, Samantha J.
; APPLICANT: Deede, James


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QY 986 TTCAGCATGTGTCCCTGTGCAACCACTCAACCGCTGCTGTATGAGAAGTGCACCTG 1045
DB 600 TTCAGCATGTGTCCCTGTGCAACCACTCAACCGCTGCTGTATGAGAAGTGCACCTG 659
QY 1046 AGCCGGATGAGAGCACTGAGGAAGTGTGACATGAGAGGAGCATGCGCAGAGG 1105
DB 660 AGCCGGATGAGAGCACTGAGGAAGTGTGACATGAGAGGAGCATGCGCAGAGG 719
QY 1106 AAAGCCCTTCAACCAAGAGAGAGAGCACTTCTAACTGGCTGACTTGCAGTGGCC 1165
DB 720 AAAGCCCTTCAACCAAGAGAGAGAGCACTTCTAACTGGCTGACTTGCAGTGGCC 779
QY 1166 GCCAGGAGGTTGGGCCCCAGCGGGGCTCCCTTGTGTGAGCTTTTGAAGCCAGCTGAG 1225
DB 780 GCCAGGAGGTTGGGCCCCAGCGGGGCTCCCTTGTGTGAGCTTTTGAAGCCAGCTGAG 839
QY 1226 CACCAAGCACCAGGAGCTCTGTAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAG 1285
DB 840 CACCAAGCACCAGGAGCTCTGTAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAG 899
QY 1286 AGCTTGCAAGCAAGCCAGAGAGACCTGGAGCTGTGTCTTCTGTGTGAGAGGCTCC 1345
DB 900 AGCTTGCAAGCAAGCCAGAGAGACCTGGAGCTGTGTCTTCTGTGTGAGAGGCTCC 959
QY 1346 AGCATTTCCAAAGCTTTTAAATTCATTAATGAGGCTTCCGTGTGTGAGAGGCTCCAG 1405
DB 960 AGCATTTCCAAAGCTTTTAAATTCATTAATGAGGCTTCCGTGTGTGAGAGGCTCCAG 1019
QY 1406 AGCTGGGGGTGGAGTGTGAGCACTTAAGAAAACATTAAGAGACATCTCATCATCAGG 1465
DB 1020 AGCTGGGGGTGGAGTGTGAGCACTTAAGAAAACATTAAGAGACATCTCATCATCAGG 1079
QY 1466 GGTGAAGTGTGAGTGAAGGAGGCTTCTTCAAGGCTGAGGGGTTCAGAAACAGGCTCG 1525
DB 1080 GGTGAAGTGTGAGTGAAGGAGGCTTCTTCAAGGCTGAGGGGTTCAGAAACAGGCTCG 1139
QY 1526 CCAAAAATTACACAGAGAGAGAGAGCTCCCTCCATTGGGAACAGGGGTATTGAGGAAG 1585
DB 1140 CCAAAAATTACACAGAGAGAGAGAGCTCCCTCCATTGGGAACAGGGGTATTGAGGAAG 1199
QY 1586 TGAACCTTGGGTGAGAGGACCAATCTGTGACCTCCAGAACCATAGAAAGCCAGAGCT 1645
DB 1200 TGAACCTTGGGTGAGAGGACCAATCTGTGACCTCCAGAACCATAGAAAGCCAGAGCT 1259
QY 1646 CAGGCTGACCAACACCTCAACCTTCTGAGAGAGCCCATTTGGGCCCGCATGTTGTA 1705
DB 1260 CAGGCTGACCAACACCTCAACCTTCTGAGAGAGCCCATTTGGGCCCGCATGTTGTA 1319
QY 1706 TTTTGTCTATTTTAACTTCTGTGTTACCTGA 1741
DB 1320 TTTTGTCTATTTTAACTTCTGTGTTACCTGA 1355

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RESULT 14

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US-09-652-913-8169
; Sequence 8169, Apolipoprotein US/09522913
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean R.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1174-001
; CURRENT APPLICATION NUMBER: US/09/652,913
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,107
; NUMBER OF SEQ ID NOS: 10833
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8169
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1)...(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-913-8169
Query Match 58.5%; Score 1019.2; DB 25; Length 1512;
Best Local Similarity 99.1%; Pred. No. 1.2e-239;
Matches 1046; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
QY 687 TCTCTTAAGTGAAGATCCCTTCTCTGAGAGACAGAAAGCACTGGCAATA 746
DB 301 TCAGCTTAAGTGAAGATCCCTTCTCTGAGAGACAGAAAGCACTGGCAATA 360
QY 747 TCACATCAGTGAAGTTCAGACTTTGATGAGGAATTTTCACCATACGAGGAGCTGCCA 806
DB 361 TCACATCAGTGAAGTTCAGACTTTGATGAGGAATTTTCACCATACGAGGAGCTGCCA 420
QY 807 AGGACTTTATTCGGAAGCTTCTGTGTTAAAGAGCCCGGAAAGGCTCACATCCAGAG 866
DB 421 AGGACTTTATTCGGAAGCTTCTGTGTTAAAGAGCCCGGAAAGGCTCACATCCAGAG 479
QY 867 CTCTCAGACACCCCTGGATCAGCCCGGTGAGCAACAGCAAGCCATGTG- CGACGGAG 925
DB 480 CTCTCAGACACCCCTGGATCAGCCCGGTGAGCAACAGCAAGCCATGTGCGCAGGAG 539
QY 926 TCTGTGTCAATCTGAGAACTTCAAGAGCAGTATGTCCGACGGCGGTGGAAGCTTTCC 985
DB 540 TCTGTGTCAATCTGAGAACTTCAAGAGCAGTATGTCCGACGGCGGTGGAAGCTTTCC 529
QY 986 TTTGAGCATGCGTGTCCCGTCAACCACTCACCCGCTCGCTGATGAAGAGTGCACCTG 1045
DB 600 TTTGAGCATGCGTGTCCCGTCAACCACTCACCCGCTCGCTGATGAAGAGTGCACCTG 659
QY 1046 AGCCGGATGAGAGCACTGAGGAACCTGTGAGAGTGAACCTGAGAGAGCATTCGCCAGAG 1105
DB 660 AGCCGGATGAGAGCACTGAGGAACCTGTGAGAGTGAACCTGAGAGAGCATTCGCCAGAG 719
QY 1106 AAAGCCCTTCAACCAAGAGAGAGAGAGCACTTCTTAATGGGCTGACCTGAGTGGCC 1165
DB 720 AAAGCCCTTCAACCAAGAGAGAGAGAGCACTTCTTAATGGGCTGACCTGAGTGGCC 779
QY 1166 GCCAGGAGGTTTGGGCCCCAGCGGGGCTCCCTTGTGTGAGCACTTTTGAAGCCAGCTCAG 1225
DB 780 GCCAGGAGGTTTGGGCCCCAGCGGGGCTCCCTTGTGTGAGCACTTTTGAAGCCAGCTCAG 839
QY 1226 CACCAAGCACCAGGAGCTCTGTAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAG 1285
DB 840 CACCAAGCACCAGGAGCTCTGTAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAG 899
QY 1286 AGCTTGCAAGCAAGCCAGAGAGACCTGGAGCTGTGTCTTCTGTGTGAGAGGCTCC 1345
DB 960 AGCTTGCAAGCAAGCCAGAGAGACCTGGAGCTGTGTCTTCTGTGTGAGAGGCTCC 959
QY 1346 AGCATTTCCAAAGCTTTTAAATTCATTAATGAGGCTTCTGTGTGAGAGGCTCCAG 1405
DB 980 AGCATTTCCAAAGCTTTTAAATTCATTAATGAGGCTTCTGTGTGAGAGGCTCCAG 1019
QY 1406 AGCTGGGGGTGGAGTGTGAGCACTTAAGAAAACATTAAGAGACATCTCATCATCAGG 1465
DB 1020 AGCTGGGGGTGGAGTGTGAGCACTTAAGAAAACATTAAGAGACATCTCATCATCAGG 1079
QY 1466 GGTGAAGTGTGAGTGAAGGAGGCTTCTTCAAGGCTGAGGGGTTCAGAAACAGGCTCG 1525
DB 1080 GGTGAAGTGTGAGTGAAGGAGGCTTCTTCAAGGCTGAGGGGTTCAGAAACAGGCTCG 1139
QY 1526 CCAAAAATTACACAGAGAGAGAGAGCTCCCTCCATTGGGAACAGGGGTATTGAGGAAG 1585
DB 1140 CCAAAAATTACACAGAGAGAGAGAGCTCCCTCCATTGGGAACAGGGGTATTGAGGAAG 1199
QY 1586 TGAACCTTGGGTGAGAGGACCAATCTGTGACCTCCAGAAACATAGAAAGCCAGAGCT 1645
DB 1200 TGAACCTTGGGTGAGAGGACCAATCTGTGACCTCCAGAAACATAGAAAGCCAGAGCT 1259
QY 1646 CAGGCTGACCAACACCTCAACCTTCTGAGAGAGCCCATTTGGGCCCGCATGTTGTA 1705

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Db 1260 CAGGTCGACCAACCTAGACCTTCTGAAAGCAGCCCATCTGCGCCGCCATGTTGAA 1319
Qy 1706 TTTGCTCATTTTATTAATACTTGTGTTTACCTGA 1741
Db 1320 TTTGCTCATTTTATTAATACTTGTGTTTACCTGA 1355
RESULT 15
US-09-652-917-2793
; Sequence 2793, Application US/09652917
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600,1170-001
; CURRENT APPLICATION NUMBER: US/09/652,917
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,422
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 3855
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2793
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-917-2793

Query March 58.5%; Score 1019.2; DB 25; Length 1512;

Best Local Similarity 99.1%; Pred. No. 1.2e-239;

Matches 1046; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

Qy 687 TCCTCTTAAGTGAAGCATCCCTTCTCTGGAGACACGAAGAGAAACATCGCAATA 746
Db 301 TCAGTTAAGTGAAGCATCCCTTCTCTGGAGACACGAAGAGAAACATCGCAATA 360
Qy 747 TCACATCAGTGAAGTACGACTTTGATGAAATTTCTCAGCCATACGAGCGAGTGC 806
Db 361 TCACAGCAGTGAAGTACGACTTTGATGAAATTTCTCAGCCATACGAGCGAGTGC 420
Qy 807 AGGACTTATTCGGAAGCTTCTGTTAAAGAACCCGGAACGCTCAATCCAAAGG 866
Db 421 AGGACTTATTCGGAAGCTTCTGTTAAAGAACCCGGAACGCTCAATCCAAAGG 479
Qy 867 CTCTCAGACACCCCTGATACGCGCGGTGAACAACGAAAGCCATGGTG--CGAGGGAG 925
Db 480 CTCTCAGACACCCCTGATACGCGCGGTGAACAACGAAAGCCATGGTGCGGAGAG 539
Qy 926 TCTGTGTCAACTCTGAGAACTTCAGAAAGCATATGTCGCGAGCGGTGAAGCTTTC 985
Db 540 TCTGTGTCAACTCTGAGAACTTCAGAAAGCATATGTCGCGAGCGGTGAAGCTTTC 599
Qy 986 TTCAGCATGTCGTCTCTGTGCAACCACTCACCCGCTGCTGATGAAGAAGTGCACCTG 1045
Db 600 TTCAGCATGTCGTCTCTGTGCAACCACTCACCCGCTGCTGATGAAGAAGTGCACCTG 659
Qy 1046 AGGCGGATGAGGACCTGAGAACTGTAGAGTGAACCTGAGGAGAGATGCGCGAGAG 1105
Db 660 AGGCGGATGAGGACCTGAGAACTGTAGAGTGAACCTGAGGAGAGATGCGCGAGAG 719
Qy 1106 AAAGCCCTCCACCCAGGAGAGAGAGACACTTCTAACTGGCTGACCTGAGTGGCC 1165
Db 720 AAAGCCCTCCACCCAGGAGAGAGAGACACTTCTAACTGGCTGACCTGAGTGGCC 779
Qy 1166 GCCAGGAGGTTTGGGCCAGGGGGCTCTCTTGTGTGAACCTTTGAGCCAGCTCAG 1225
Db 780 GCCAGGAGGTTTGGGCCAGGGGGCTCTCTTGTGTGAACCTTTGAGCCAGCTCAG 839

Qy 1226 CACCAGCACCCGGGGCTCTGAGCATTTTGAAGAGATGGGCCCAAGAAATTCAGAG 1285
Db 840 CACCAGCACCCGGGGCTCTGAGCATTTTGAAGAGATGGGCCCAAGAAATTCAGAG 899
Qy 1286 AGCTTGAGGAGGACGAGAGACCTTGGAGCTGTGCTTCTGTGAGAGAGGCTCC 1345
Db 900 AGCTTGAGGAGGACGAGAGACCTTGGAGCTGTGCTTCTGTGAGAGAGGCTCC 959
Qy 1346 AGCATTTCCAAAGCTCTAATTTCTCATAAATGGGCTTCTCTGTCTGCATCTCAG 1405
Db 960 AGCATTTCCAAAGCTCTAATTTCTCATAAATGGGCTTCTCTGTCTGCATCTCAG 1019
Qy 1406 AGCTGGGGTGGAGTGTGACCTTAGAAAACAATATTAAGACATCTCATACAGG 1465
Db 1020 AGCTGGGGTGGAGTGTGACCTTAGAAAACAATATTAAGACATCTCATACAGG 1079
Qy 1466 GGTGAAGTCAAGTGAAGGACGCTTCTTCAAGGCTGAGGGGTTCAAAACAGCTGG 1525
Db 1080 GGTGAAGTCAAGTGAAGGACGCTTCTTCAAGGCTGAGGGGTTCAAAACAGCTGG 1139
Qy 1526 CCAAAAATTACACAGAGAGACAGAGTCTCCCATTTGGGAAACAGGCTGATGAGGAA 1585
Db 1140 CCAAAAATTACACAGAGAGACAGAGTCTCCCATTTGGGAAACAGGCTGATGAGGAA 1199
Qy 1586 TGAACCTTGGGTGAGGAGCAATCTGTGACCTCCAGAACATGGAAGCAGAGAGT 1645
Db 1200 TGAACCTTGGGTGAGGAGCAATCTGTGACCTCCAGAACATGGAAGCAGAGAGT 1259
Qy 1646 CAGGTCGACCAACCTCAGACCTTGTGAAGCAGGCCATTGTGCGCCGCAATGTTGTA 1705
Db 1260 CAGGTCGACCAACCTCAGACCTTGTGAAGCAGGCCATTGTGCGCCGCAATGTTGTA 1319
Qy 1706 TTTGCTCATTTTATTAATACTTGTGTTTACCTGA 1741
Db 1320 TTTGCTCATTTTATTAATACTTGTGTTTACCTGA 1355

Search completed: Apr-11 4, 2003, 22:30:05
Job time : 5391.24 secs

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|----|-----|--|-----|
| Qy | 1 | GACCGCGGACGTAGGCTCCCGCGAATTGATATGTCACAGCCCTCAATGAGAGTCCAA | 60 |
| Db | 8 | GACCGCGGACGTAGGCTCCCGCGAATTGATATGTCACAGCCCTCAATGAGAGTCCAA | 67 |
| Qy | 61 | CATGAGCCATTCAAGCAGCAGAAAGTGTGAGACTTTATGATCTCGAGAGGAGCTGG | 120 |
| Db | 68 | CATGAGCCATTCAAGCAGCAGAAAGTGTGAGACTTTATGATCTCGAGAGGAGCTGG | 122 |
| Qy | 121 | GAGTGGCCAGTTTCCCATTCGTGAAGAGTGC CGGAGAAAGCA CGGGGCTTGATGC | 180 |
| Db | 128 | GAGTGGCCAGTTTCCCATTCGTGAAGAGTGC CGGAGAAAGCA CGGGGCTTGATGC | 187 |
| Qy | 181 | AGCCAA GTTCATCAAGAA GCGGCGAGAGCCCGGCGCGGTGTGAGCCGGGAGGA | 240 |
| Db | 188 | AGCCAA GTTCATCAAGAA GCGGCGAGAGCCCGGCGCGGTGTGAGCCGGGAGGA | 247 |
| Qy | 241 | GATGGAACGGGAGGTGAGCATCTCTGCGGCGAGTCTGCACACAAATCTCAACGCTGCA | 300 |
| Db | 248 | GATGGAACGGGAGGTGAGCATCTCTGCGGCGAGTCTGCACACAAATCTCAACGCTGCA | 307 |
| Qy | 301 | CGACGTCATAGAAACGCGACCGAGCTGTGGACATCTTGAGCTAGTGTCTGGAGAGA | 360 |
| Db | 308 | CGACGTCATAGAAACGCGACCGAGGTGTGCTCATCTTGAGCTAGTGTCTGGAGAGA | 366 |

Qy 361 GCTCTTGATTTTCCGCGCCAGAAAGTCACTGATGAGAGGAGCCACCAAGCTTCAT 420
Db 368 GCTCTTGATTTTCCGCGCCAGAAAGTCACTGATGAGAGGAGCCACCAAGCTTCAT 427
Qy 421 TAAGCAGATTCCTGATGAGGATGAACTACCTTCAACAAAGAAATTTGCTCACTTGAATCT 480
Db 428 TAAGCAGATTCCTGATGAGGATGAACTACCTTCAACAAAGAAATTTGCTCACTTGAATCT 487
Qy 481 CAAGCCAGAAATTAATGTTGTTAGACAAGAAATTTCCATTCACACATCAAGCTGAT 540
Db 488 CAAGCCAGAAATTAATGTTGTTAGACAAGAAATTTCCATTCACACATCAAGCTGAT 547
Qy 541 TGACTTTGGTCTGCTCAAGAAATGAAAGTGAATGAATTAATTAATTTTGGAGC 600
Db 548 TGACTTTGGTCTGCTCAAGAAATGAAAGTGAATGAATTAATTAATTTTGGAGC 607
Qy 601 GCCGGAATTTGTTGCTCCAGAAATTTGTAACACAGAGCCCTGGGCTGGAAGCTGACAT 660
Db 608 GCCGGAATTTGTTGCTCCAGAAATTTGTAACACAGAGCCCTGGGCTGGAAGCTGACAT 667
Qy 661 GTGGAGCATAGGCGTCATACCTACCTCTTAAGTGGAGCATCCCTTTCCTGGAGA 720
Db 668 GTGGAGCATAGGCGTCATACCTACCTCTTAAGTGGAGCATCCCTTTCCTGGAGA 727
Qy 721 CACGAGCAGAGAAACACTGGCAAAATATCAATCAGTGAATTCAGCTTTGATGAGAAAT 780
Db 728 CACGAGCAGAGAAACACTGGCAAAATATCAATCAGTGAATTCAGCTTTGATGAGAAAT 787
Qy 781 CTTTACCCATACAGAGAGAGTGGCCAAAGACTTTATTCGAAAGCTTCTGTTAAAGAGC 840
Db 788 CTTTACCCATACAGAGAGAGTGGCCAAAGACTTTATTCGAAAGCTTCTGTTAAAGAGC 847
Qy 841 CCGGAAACGGCTCAACATCCAAAGGCTCTCAGACACCCCTGATCAAGCCGCTGAGCA 900
Db 848 YCCGAAACGGCTCAACATCCAAAGGCTCTCAGACACCCCTGATCAAGCCGCTGAGCA 907
Qy 901 CCAGCAAGCCATGCTGAGAGAGAGTCTGTGTCATCTGGAGAACTTCAGAGAGAGTA 960
Db 908 CCAGCAAGCCATGCTGAGAGAGAGTCTGTGTCATCTGGAGAACTTCAGAGAGAGTA 967
Qy 961 TGTCCGAGGCGGTGAGAGCTTCTCCTCAGACATCGTGTCCCTGTGCAACCACTCACCG 1020
Db 968 TGTCCGAGGCGGTGAGAGCTTCTCCTCAGACATCGTGTCCCTGTGCAACCACTCACCG 1027
Qy 1021 CTGCTGATGAGAAAGTGAAGCTGAGAGCGGATGAGAGCTTGAAGAACTGTGAGAGTA 1080
Db 1028 CTGCTGATGAGAAAGTGAAGCTGAGAGCGGATGAGAGCTTGAAGAACTGTGAGAGTA 1087
Qy 1081 CACTGAGAGAGACATCGCCAGAGAGAAAGCCCTCAACCCAGAGAGAGAGAGCACTTC 1140
Db 1088 CACTGAGAGAGACATCGCCAGAGAGAAAGCCCTCAACCCAGAGAGAGAGAGCACTTC 1147
Qy 1141 CTAATGCGCTGACCTGAGAGTGCAGAGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 1200
Db 1148 CTAATGCGCTGACCTGAGAGTGCAGAGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGG 1207
Qy 1201 GTGCAAGCTTTTGAAGCCAGCTCAGACACCAAGCCGAGGCTTCTGAGCACTTGAAGA 1260
Db 1208 GTGCAAGCTTTTGAAGCCAGCTCAGACACCAAGCCGAGGCTTCTGAGCACTTGAAGA 1267
Qy 1261 GAGATGGGCGCAAGAAATTCAGAAAGCTTGAAGAGCAAGCCAGAGAGACCTTGGAGCTGT 1320
Db 1268 GAGATGGGCGCAAGAAATTCAGAAAGCTTGAAGAGCAAGCCAGAGAGACCTTGGAGCTGT 1327
Qy 1321 GGCTGTCTTGTGAGAGAGGCTCAGACATTCCAAAGCTTTAATTTCTCATAAATGG 1380
Db 1328 GGCTGTCTTGTGAGAGAGGCTCAGACATTCCAAAGCTTTAATTTCTCATAAATGG 1387
Qy 1381 GCTTTCTCTCTGCTGCAATCTCAGAGCTGGGAGTGGAGTGGAGCTTGAAGAAACAT 1440
Db 1388 GCTTTCTCTCTGCTGCAATCTCAGAGCTGGGAGTGGAGTGGAGCTTGAAGAAACAT 1447
Qy 1441 ATAAAGACATCTCATCATCAAGGAGTGAAGTCAAGTAAGGAGCTTCTTCAAGG 1500

Db 1448 ATAAAGACATCTCATCATCAAGGAGTGAAGTCAAGTAAGGAGCTTCTTCAAGG 1507
Qy 1501 CTGAGGGGTTAGAAACCAAGCTTGCCCAAAATTTACACAGAGAGAGAGGCTTCCCCA 1560
Db 1508 CTGAGGGGTTAGAAACCAAGCTTGCCCAAAATTTACACAGAGAGAGAGGCTTCCCCA 1567
Qy 1561 TTGGGAACAGGGTGAATTTGGAAGAGTGAACCTTGGGTGAGAGGCAATCCTGTGACT 1620
Db 1568 TTGGGAACAGGGTGAATTTGGAAGAGTGAACCTTGGGTGAGAGGCAATCCTGTGACT 1627
Qy 1621 CCAGAACCATGAGAACCAAGAGCTGAGCTGACCAACCTTCAAGCTTCTGAAAGAGC 1680
Db 1628 CCAGAACCATGAGAACCAAGAGCTGAGCTGACCAACCTTCAAGCTTCTGAAAGAGC 1687
Qy 1681 CCAATGCTGCGCCCATGTTGTAATTTTGTCAATTTTAACTTCTGTTTACTG 1740
Db 1688 CCAATGCTGCGCCCATGTTGTAATTTTGTCAATTTTAACTTCTGTTTACTG 1747
Qy 1741 A 1741
Db 1748 A 1748

RESULT 2
US-09-724-676-34736/c
Sequence 34736, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181, 4 Compugen
CURRENT APPLICATION NUMBER: US/09/724, 676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34736
LENGTH: 1442
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-34736

Query Match 68.9%; Score 1199.8; DB 6; Length 1442;
Best Local Similarity 99.5%; Pred. No. 3,5e-296;
Matches 1201; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACCGCGCAGCTCAGAGCTCCCGCGAATGTATGATTCAGGCTTCAATGAGAGTCCAAA 60
Db 1435 GACCGCGCAGCTCAGAGCTCCCGCGAATGTATGATTCAGGCTTCAATGAGAGTCCAAA 1376
Qy 61 CATGAGCCATTCAAGCAGAGAGTGGAGAGCTTTTATGACATCGGAGAGAGCTGGG 120
Db 1375 CATGAGCCATTCAAGCAGAGAGTGGAGAGCTTTTATGACATCGGAGAGAGCTGGG 1316
Qy 121 GAGTGGCCAGTTTGCATCTGTAAGAAATGCGGAGAGAGACAGGGGCTTGAATGC 180
Db 1315 GAGTGGCCAGTTTGCATCTGTAAGAAATGCGGAGAGAGACAGGGGCTTGAATGC 1256
Qy 181 AGCCAAATTCATCAAGAAAGCGCAGAGCGCGGCGAGCGCGCGGTGTGAGCCGAGAGA 240
Db 1255 AGCCAAATTCATCAAGAAAGCGCAGAGCGCGGCGAGCGCGCGGTGTGAGCCGAGAGA 1196
Qy 241 GATCGAGCGGAGTGAAGATCTGCGGAGGCTGTGACACCAATGTATCATCAGCTGCA 300
Db 1195 GATCGAGCGGAGTGAAGATCTGCGGAGGCTGTGACACCAATGTATCATCAGCTGCA 1136
Qy 301 CGACGTCTATGAGAAACCGCAGCAGAGTGTGACATCTTGAAGTATGTCTTGAAGAGA 360
Db 1135 CGACGTCTATGAGAAACCGCAGCAGAGTGTGACATCTTGAAGTATGTCTTGAAGAGA 1076
Qy 361 GCTCTTGATTTCTGCGCCAGAGAGTCACTGAGTGAAGAGAGGCGCACCAAGCTTCAT 420
Db 1075 GCTCTTGATTTCTGCGCCAGAGAGTCACTGAGTGAAGAGAGGCGCACCAAGCTTCAT 1016

| | | | |
|----|------|---|------|
| Oy | 421 | TAAGAGATCTGGATGGGGTGAACCTACCTTCAACAAAGAAAATGGCTACCTTGGATC | 480 |
| Db | 1015 | TAAAGCATCTCGATGGGGTGAACCTACCTTCAACAAAGAAAATGGCTACCTTGGATC | 956 |
| Oy | 481 | CAAGCCAGAAAACTATATGTTGTTAGAAGAAATATTTCCATTCCACATCAAGCTGAT | 540 |
| Db | 955 | CAAGCCAGAAAACTATATGTTGTTAGAAGAAATATTTCCATTCCACATCAAGCTGAT | 896 |
| Oy | 541 | TGACTTTGGCTTGGCTACCGAAAATGAGATGAGATTTGAATTTAAGAAATATTTTGGGAC | 600 |
| Db | 895 | TGACTTTGGCTTGGCTACCGAAAATGAGATGAGATTTGAATTTAAGAAATATTTTGGGAC | 836 |
| Oy | 601 | GCCGGAAATTTTGTCTCCAGAAATTTGAACTACGAGACCCTGGGCTGAGAGCTGACAT | 660 |
| Db | 835 | GCCGGAAATTTGTCTCCAGAAATTTGAACTACGAGACCCTGGGCTGAGAGCTGACAT | 776 |
| Oy | 661 | GTGAGCATAGGCGCTCATCACTTACATCTCTTTAAGTGAAGCATCCCTTTTCTGGGAGA | 720 |
| Db | 775 | GTGAGCATAGGCGCTCATCACTTACATCTCTTTAAGTGAAGCATCCCTTTTCTGGGAGA | 716 |
| Oy | 721 | CACGAAAGAGAAAACATGGCAAAATACATATAGAGATTCAGATTTGATGAGAGATT | 780 |
| Db | 715 | CACGAAAGAGAAAACATGGCAAAATACATACAKAGATGATTCAGATTTGATGAGAGAAAT | 656 |
| Oy | 781 | CTTCAGCCATACGAGCGAGCTGGCCAAAGACCTTATTTCCGAAAGCTTCTGTTAAAGAAC | 840 |
| Db | 655 | CTTCAGCCAKACGAGCGAGCTGGCCAAAGACCTTATTTCCGAAAGCTTCTGTTAAAGAAC | 596 |
| Oy | 841 | CCGGAACCGCTCAACAATCCAGAGGCTTCAAGACACCCCTGGATCACGCCGGTGAACAA | 900 |
| Db | 595 | CCGGAACCGGCTCAACAATCCAGAGGCTTCAAGACACCCCTGGATCACGCCGGTGAACAA | 536 |
| Oy | 901 | CCAGAAAGCCATGTGTGGAGCGGGAGTGTGGTCATCTGGAGAACTTGAGGAACAGTA | 960 |
| Db | 535 | CCAGCAAGCCATGTGTGGAGCGGGAGTGTGGTCATCTGGAGAACTTGAGGAACAGTA | 476 |
| Oy | 961 | TGTCCGAGGCGGTGAAGCTTTCTTCAGCATCGTGTCCCTGTGCAACACCTCACCGG | 1020 |
| Db | 475 | TGTCCGAGGCGGTGAAGCTTTCTTCAGCATCGTGTCCCTGTGCAACACCTCACCGG | 416 |
| Oy | 1021 | CTCCGCTGATGAAAGAGGTGCACTCGAGGCGGGATGAGAACTTGAGGAATGTGAGAGTGA | 1088 |
| Db | 415 | CTCCGCTGATGAAAGAGGTGCACTCGAGGCGGGATGAGAACTTGAGGAATGTGAGAGTGA | 356 |
| Oy | 1081 | CACGTAGAGAGACATTCGCCAGAGAGAAAGCCTTCCACCACGGAGGAGAGACGACACTTC | 1148 |
| Db | 355 | CACGTAGAGAGACATTCGCCAGAGAGAAAGCCTTCCACCACGGAGGAGAGACGACACTTC | 296 |
| Oy | 1141 | CTAACTGGCCTGACCTGACAGTGGCCGCCAGAGAGGTTTGGGCCACAGCGGGAGCTCCCTTCT | 1200 |
| Db | 295 | CTAACTGGCCTGACCTGACAGTGGCCGCCAGAGAGGTTGTTGGGCCACAGCGGGAGCTCCCTTCT | 236 |
| Oy | 1201 | GTGCAGA 1207 | |
| Db | 235 | GTGCAGA 229 | |

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RESULT 3
US-09-724-676A-34736/C
; Sequence 34736, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34736
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-34736

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| | | | | |
|----------------------------|--------|---------------------|-----------|--------------|
| Query Match | 68.9% | Score 1199.8; | DB 6; | Length 1442; |
| Best Local Similarity | 99.5%; | Pred. No. 3.5e-296; | | |
| Matches 1201; Conservative | 2; | Mismatches 4; | Indels 0; | Gaps 0; |

| | | | |
|----|------|---|------|
| QY | 1 | GACCGCGGACAGCTCAGGCTCCCGCCCAATGTATGTTCAAGGCGCTCAATAGAGAGTCCAA | 60 |
| Db | 1435 | GACCGCGGACAGCTCAGGCTCCCGCCCAATGTATGTTCAAGGCGCTCAATAGAGAGTCCAA | 1378 |
| QY | 61 | CATGAGCATTCAGACGACGAAAGGTGAGAGCTTTATATGACATCGAGAGAGAGCTGG | 120 |
| Db | 1375 | CATGAGCATTCAGACGACGAAAGGTGAGAGCTTTATATGACATCGAGAGAGAGCTGG | 1318 |
| QY | 121 | GAGTGGCCAGTTTGGCCATTCGTGAAAGAAAGTCCGGGAGAAAGACACAGGGGCTTGAGTAGC | 180 |
| Db | 1315 | GAGTGGCCAGTTTGGCCATTCGTGAAAGAAAGTCCGGGAGAAAGACACAGGGGCTTGAGTAGC | 1255 |
| QY | 181 | AGCCAAAGTTTCATCAAGAAAGCGGACGAGACCGGGCGAGCCCGCGGTGTGACCGCCGAGGA | 240 |
| Db | 1255 | AGCCAAAGTTTCATCAAGAAAGCGGACGAGACCGGGCGAGCCCGCGGTGTGACCGCCGAGGA | 1195 |
| QY | 241 | GATGAGCGGGAGGTGAGCATCTCTGGGCGAGGTGCTGACACCAATGTCATACGCTGCA | 300 |
| Db | 1195 | GATGAGCGGGAGGTGAGCATCTCTGGGCGAGGTGCTGACACCAATGTCATACGCTGCA | 1185 |
| QY | 301 | CGAGCTCATATGAAACCGCACCGACGTGTGCAATCCTTGAGCTATAGTGTCTGGAGGAGA | 360 |
| Db | 1135 | CGAGCTCATATGAAACCGCACCGACGTGTGCAATCCTTGAGCTATAGTGTCTGGAGGAGA | 1078 |
| QY | 361 | GCTCTTCGATTTCTGTGCGCCAGAAAGAGTCACTGAGTGAAGAGAGGCCACAGCTTAT | 420 |
| Db | 1075 | GCTCTTCGATTTCTGTGCGCCAGAAAGAGTCACTGAGTGAAGAGAGGCCACAGCTTAT | 1018 |
| QY | 421 | TAAAGCATCTCGATGGGGTGAATCTTCCACACAAAGAAATTTGCTCACTTTGATCT | 480 |
| Db | 1015 | TAAAGCATCTCGATGGGGTGAATCTTCCACACAAAGAAATTTGCTCACTTTGATCT | 956 |
| QY | 481 | CAAGCCAGAAACCTTATGTTGTTAGCAAGAAATATTCCTTCCACACATCAAGCTAT | 540 |
| Db | 955 | CAAGCCAGAAACCTTATGTTGTTAGCAAGAAATATTCCTTCCACACATCAAGCTAT | 896 |
| QY | 541 | TGACTTTGGTCTGGCTCAGCAAAATAGAAAGTGAATTAAGAAATATTTTGGAC | 600 |
| Db | 895 | TGACTTTGGTCTGGCTCAGCAAAATAGAAAGTGAATTAAGAAATATTTTGGAC | 836 |
| QY | 601 | GCCGGAATTTGTTCTCCAGAAATTTGTGAATCTACAGGCCCTTGGGTCTGAGAGCTGACAT | 660 |
| Db | 835 | GCCGGAATTTGTTCTCCAGAAATTTGTGAATCTACAGGCCCTTGGGTCTGAGAGCTGACAT | 776 |
| QY | 661 | GTGGAGCATAGGCGGTATCTCAATCCCTTAAATGAGAGATCCCTTTCCTGGGAGA | 720 |
| Db | 775 | GTGGAGCATAGGCGGTATCTCAATCCCTTAAATGAGAGATCCCTTTCCTGGGAGA | 716 |
| QY | 721 | CACGAGCAGGAAACACTGTGCAATATCACTACAGTGAATTACGACTTTGATGAGAAATT | 780 |
| Db | 715 | CACGAGCAGGAAACACTGTGCAATATCACTACAGTGAATTACGACTTTGATGAGAAATT | 656 |
| QY | 781 | CTTCAGGCATTCAGAGCGAGCTGGCCAAAGACTTTATTCGAAAGCTTTGTGTTAAAGAC | 840 |
| Db | 655 | CTTCAGGCATTCAGAGCGAGCTGGCCAAAGACTTTATTCGAAAGCTTTGTGTTAAAGAC | 596 |
| QY | 841 | CCGGAACCGGTCTCAATTCACAAGAGGTCTACAGACACCCCTGATACAGCCGGTGAACA | 900 |
| Db | 535 | CCGGAACCGGTCTCAATTCACAAGAGGTCTCTCAGACACCCCTGATACAGCCGGTGAACA | 536 |
| QY | 901 | CCAGCAAGCCATGTGTGCGACGGGAGTCTGTGTCAATCTGAGAACTTCAGAGACAGTA | 960 |
| Db | 535 | CCAGCAAGCCATGTGTGCGACGGGAGTCTGTGTCAATCTGAGAACTTCAGAGACAGTA | 476 |
| QY | 961 | TGTCGCGAGCGGTGGAAGCTTTTCCTTACAGATCGTGTCCCTGTGCAACACTCACCG | 1020 |
| Db | 475 | TGTCGCGAGCGGTGGAAGCTTTTCCTTACAGATCGTGTCCCTGTGCAACACTCACCG | 416 |

QY 1021 CTCGCTGATGAAGAAGTGCACCTGAGGCGGATGATGAGACCTGAGAACTGTGAGAGTGA 1080
 Db 415 CTCGCTGATGAAGAAGTGCACCTGAGGCGGATGATGAGACCTGAGAACTGTGAGAGTGA 356
 QY 1081 CACTGAGAGAGACATCGCCAGAGAGAAAGCCCTCCACCACGAGAGAGAGACAGACCTC 1140
 Db 355 CACTGAGAGAGACATCGCCAGAGAGAAAGCCCTCCACCACGAGAGAGAGAGACAGACCTC 296
 QY 1141 CTAACCTGCTGACCTGACAGTGGCCGCGAGAGAGGTTGGGCGGAGGAGGCTCCCTTCT 1200
 Db 295 CTAACCTGCTGACCTGACAGTGGCCGCGAGAGAGGTTGGGCGGAGGAGGCTCCCTTCT 236
 QY 1201 GTGCAGA 1207
 Db 235 GTGCAGA 229

RESULT 4
 US-10-144-771-3361
 ; Sequence 3361, Application US/10144771
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig
 ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
 ; FILE REFERENCE: CL001321
 ; CURRENT APPLICATION NUMBER: US/10/144,771
 ; CURRENT FILING DATE: 2002-05-15
 ; NUMBER OF SEQ ID NOS: 47235
 ; SEQ ID NO 3361
 ; LENGTH: 1732
 ; TYPE: DNA
 ; ORGANISM: HUMAN
 US-10-144-771-3361

Query Match 59.3%; Score 1032.4; DB 8; Length 1732;
 Best Local Similarity 83.8%; Pred. No. 2.3e-253;
 Matches 1263; Conservative 0; Mismatches 186; Indels 59; Gaps 6;

QY 8 GCAGCTCAGCCTCCCGCGATGTTGATGTTCCAGGCTCAATGAGAGTCCAAACATGAGAG 67
 Db 91 GCAGCTCAGCCTCCCGCGATGTTGATGTTCCAGGCTCAATGAGAGTCCAAACATGAGAG 150
 QY 68 CCATTCAAGCAGAGAGTGGAGAGCTTTTATGACATCCGAGAGAGAGCTGGGAGTGGC 127
 Db 151 ACCTTCAAGCAGAGAGTGGAGAGCTTTTATGACATCCGAGAGAGAGCTGGGAGTGGC 210
 QY 128 CAGTTTGCATCTGAGAGAGTGCCTGGAGAGAGCAAGGAGGCTTGAATGAGAGCCAG 187
 Db 211 CAGTTTGCATCTGAGAGAGTGCCTGGAGAGAGCAAGGAGGCTTGAATGAGAGCCAG 270
 QY 188 TTTCATCAAGAGCGGAGAGCGGCGGAGCGGCGGCTGTGAGCCGAGAGAGATCGAG 247
 Db 271 TTTCATCAAGAGCGGAGAGCGGCGGAGCGGCGGCTGTGAGCCGAGAGAGATCGAG 330
 QY 248 CGGAGTGGAGATCTGCGGAGAGTGTGACCAATGTATCATACGCTGACGAGCTC 307
 Db 331 CGGAGTGGAGATCTGCGGAGAGTGTGACCAATGTATCATACGCTGACGAGCTC 390
 QY 308 TATGAGAACCGGACCGAGCTGTGACATCTTGAAGTAAAGTGTGAGAGAGAGCTCTTC 367
 Db 391 TATGAGAACCGGACCGAGCTGTGACATCTTGAAGTAAAGTGTGAGAGAGAGCTCTTC 450
 QY 368 GATTTTCCGAGCCAGAGAGTCACTGAGTGGAGAGAGGACACAGCTTCAATTAAGAG 427
 Db 451 GATTTTCCGAGCCAGAGAGTCACTGAGTGGAGAGAGGACACAGCTTCAATTAAGAG 510
 QY 428 ATCTGATGGAGTGAATTAACCTTCAACAAAGAAATTTGCTCACTTTGATCTCAAGCA 487
 Db 511 ATCTGATGGAGTGAATTAACCTTCAACAAAGAAATTTGCTCACTTTGATCTCAAGCA 570
 QY 488 GAAACATTAATGTTGTTAACAAGAAATATTCATTTCCACATCAAGCTGATTAAGCTTT 547
 Db 571 GAAACATTAATGTTGTTAACAAGAAATATTCATTTCCACATCAAGCTGATTAAGCTTT 630

QY 548 GGTCTGCTACGAAATATGAAGATGAGATTGAATTAAGAAATATTTTGGAGCCCGGAA 607
 Db 631 GGTCTGCTACGAAATATGAAGATGAGATTGAATTAAGAAATATTTTGGAGCCCGGAA 690
 QY 608 TTTGTTGCTCCAGAAATTTGTAACTACAGAGCCCTGGTCTGAGAGGCTGACATGTGAGAGC 667
 Db 691 TTTGTTGCTCCAGAAATTTGTAACTACAGAGCCCTGGTCTGAGAGGCTGACATGTGAGAGC 746
 QY 668 ATAGGCTATCACTCACTCTCTTAAGTGGAGATCCCTTCTGAGAGACAGAG 727
 Db 747 -----TCTAAGTGGAGGCTCCCTTCTGAGAGACAGAA 783
 QY 728 CAGAAACACTGCAAAATATCAATCAGTAACTGATGAGAGAAATTTCTTACG 787
 Db 784 CAGAAACCTTGGCAAAATATCACTGATGAGTACGATTTGATGAGAGAAATTTCTTACG 843
 QY 788 CATACAGAGAGCTGGCCAGAGCTTTATTCGGAAGCTTGGTTAAAGAGACCCGAGAA 847
 Db 844 CAGACAGAGAGCTGGCCAGAGCTTTATTCGGAAGCTTGGTTAAAGAGACCCGAGAA 903
 QY 848 CGGCTCAAAATCCAGAGGCTCTCAGACACCCCTGATCAGCCGATGAGACAGCAA 907
 Db 904 CGGCTCAAAATCCAGAGGCTCTCAGACATCCCTGATCAGCCGATGAGACAGCAA 963
 QY 908 GCGATGCTGCGAGGAGTCTGTGCTAACTGAGAACTTCAGAGAGAGAGATATGTCGCG 967
 Db 964 GCGATGCTGCGAGGAGTCTGTGCTAACTGAGAACTTCAGAGAGAGAGATATGTCGCG 1023
 QY 968 AGCGGCTGGAAGCTTTCTTCAAGCATCGTGTCCCTGAGCAACCACTCAACCGCTGCTG 1027
 Db 1024 AGCGGCTGGAAGCTTTCTTCAAGCATCGTGTCCCTGAGCAACCACTCAACCGCTGCTG 1083
 QY 1028 ATGAAGAGTGAACCTGAGGCGGATGAGAGCTTGAAGAACTGTGAGATGACATGAG 1087
 Db 1084 ATGAAGAGTGAACCTGAGGCGGATGAGAGCTTGAAGAACTGTGAGATGACATGAG 1143
 QY 1088 GAGACATCTGCGAGAGAGAAAGCCCTTCAACCGAGAGAGAGAGACACTTCTAACTG 1147
 Db 1144 GAGACATCTGCGAGAGAGAAAGCCCTTCAACCGAGAGAGAGAGACTTCTCTAACTG 1203
 QY 1148 GCCGACCTGAGAGGCGCGCAGAGAGATTTGGGCCAGCGGGCTCTTGTGTGAGA 1207
 Db 1204 GCCGACCTGAGAGGCGCGCAGAGAGATTTGGGCCAGCGGGCTCTTGTGTGAGA 1260
 QY 1208 CTTTGAACCAAGCTCAGACACAGACCCGGGCG-----TCTGAGAGACTTTGCAAG 1259
 Db 1261 CTTTGAACCAAGCTCAGACACAGATCCAGATCCAGATCTGTGTCTTGAAGACTTTGCAAG 1320
 QY 1260 AGAGATGGGCCCAAGGAATTCAGAAAGCTTGACAGACAGCAGAGACCTTGGAGCTG 1319
 Db 1321 AGAGATGGGCCCAAGGAATTCAGAAAGCTTGACAGAACTT-----CCGAGAGCCTGGAGCTTG 1368
 QY 1320 TGGCTGTCTTGTGAGAGAGCTTCAGACATTTCCAAAGCTTTAATTTCTCATTAATG 1379
 Db 1369 TGGCTGTCTTGTGAGAGAGCTTCAGACATTTCTTGGCTTGTGAGTTCTCCAGAAACT 1428
 QY 1380 GCGTTTCTTGTCTGCAATCTTCAGAGTCTGGGGTGGAGAGTGTGAGAAATGCA 1439
 Db 1429 GCGTTTCTTGTCTGCAATCTTCAGAGCTGGAATTTGG-GTGTGACTTAAGAGAAATGGA 1487
 QY 1440 TTTAAAGG-----CATCTCATCAACAGGGGTGAAGTCAAGATTAAGAGCTTT 1491
 Db 1488 TCTCAAGAGATATCTTTTCTTTTAAACACAGGTAAAGGTAGATTAAGAGCTTT 1547
 QY 1492 CTTTCAAG 1499
 Db 1548 CTTTCAAG 1555

RESULT 5
 US-09-947-907-15358/c
 ; Sequence 15358, Application US/09947907
 ; GENERAL INFORMATION:

; APPLICANT:VENTNER, J. Craig et al.
 ; TITLE OF INVENTION: COLLECTION OF CODING REGION SINGLE
 ; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISM (CSN8) LOCATED ON EACH OF THE HUMAN
 ; TITLE OF INVENTION: CHROMOSOMES, METHODS OF DETECTION, AND USES THEREOF
 ; FILE REFERENCE: CLO000896
 ; CURRENT APPLICATION NUMBER: US/09/947,907
 ; CURRENT FILING DATE: 2003-03-17
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 21256
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15358
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-947-907-15358

| | | | | |
|---------------------------|-------|---------------------|-------|------------------|
| Query Match | 30.7% | Score 534; | DB 5; | Length 601; |
| Best Local Similarity | 99.6% | Pred. No. 3.4e-126; | | |
| Matches 534; Conservative | 1; | Mismatches | 1; | Indels 0; Gaps 0 |

| Accession | Sequence | Position |
|-----------|--|----------|
| 0y | GACTTTTGGACCCAGCTCAGACCCAGACCCGGGCGTCC | 1285 |
| 1206 | GACTTTTGGACCCAGCTCAGACCCAGACCCGGGCGTCC | 1285 |
| Db | GACTTTTGGACCCAGCTCAGACCCAGACCCGGGCGTCC | 542 |

| Qy | 1266 | GGGCCCCAAGGAATTCAGAGAGCTTGCAGGCCAAGCCAGAGACCCCTGGAGCTGTGGCTG | 1325 |
|----|------|--|------|
| Db | 541 | GGGCCCCAAGGAATTCAGAGAGCTTGCAGGCCAAGCCAGAGACCCCTGGAGCTGTGGCTG | 482 |

| QY | 1326 | TC | TC | TC | TG | GA | GA | AG | GC | TC | CA | GC | AT | TC | CC | CA | AG | CT | TA | TC | CA | TA | AA | AT | GG | CT | TT | 1385 |
|----|------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|--|----|----|----|----|----|----|----|----|------|
| QY | 1326 | TC | TC | TC | TG | GA | GA | AG | GC | TC | CA | GC | AT | TC | CC | CA | AG | CT | TA <td>TC</td> <td>CA</td> <td>TA</td> <td>AA</td> <td>AT</td> <td>GG</td> <td>CT</td> <td>TT</td> <td>1385</td> | TC | CA | TA | AA | AT | GG | CT | TT | 1385 |
| Db | 481 | TC | TC | TC | TG | GA | GA | AG | GC | TC | CA | GC | AT | TC | CC | CA | AG | CT | TA <td>TC</td> <td>CA</td> <td>TA</td> <td>AA</td> <td>AT</td> <td>GG</td> <td>CT</td> <td>TT</td> <td>422</td> | TC | CA | TA | AA | AT | GG | CT | TT | 422 |

| | | | |
|----|------|--|------|
| Dy | 1386 | CCTGTGTCGCCATCTCAGAGTCTGGGGTGGGAGTGTGACCTTAGGAAAAACAATATATAA | 1445 |
| Dz | 421 | CCCTGTGTCGCATCTCAGAGTCTGGGGTGGGAGTGTGACCTTAGGAAAAACAATATATAA | 362 |

Oy 1446 GGCATCCTCATCATCACGGGTGAAGTCAGAGTAAGCAGCCTTCTTCACAGAGCTGAG 1505
 Db 361 GGCATCCTCATCATCACGGGTGAAGTCAGAGTAAGCAGCCTTCTTCACAGAGCTGAG 302

07 1506 GGGGTT CAGAAC CCGCTGG CCAAAA ATACAC CAGAGAG ACAGAT CCTCCC ATTGGG 1565

1566 AACAGGGTGAATTGAGGAAGTAAGTGAACCTTGGGTGTGAGGGAGACCAATCTTGTGACCTCCAG 1625

QY 1626 AACCATGGAAGCCGAGACCTCAGGCTGACCAACACCTCTGACCTTCTGTAAGCAGCCCATTT 1685

1686 GCTGGCCCGCAGTGTGAATTTGGTCATTTTATTATAAAGTCTGGTTTACCTGA 1741

RESULT 6

US-05-743-016-1506
; Sequence 1966, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craia et al).

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/040016

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1966
; LENGTH: 2157
; TYPE: DNA
; ORGANISM: Human
US-03-949-016-1966

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|---------------------------|-------|---------------------|-----------|--------------|
| Query Match | 29.7% | Score 517.2; | DB 5; | Length 2157; |
| Best Local Similarity | 76.3% | Pred. No. 1,1e-121; | | |
| Matches 636; Conservative | 0; | Mismatches 198; | Indels 0; | Gaps 0 |

QY 61 CATGGAGCATTTCAAGACAGAGAAGGTGGAGACTTTTATGACATCGAGAGAGACTGGG 120
|||
Db 145 CATTGCCA GTTCAGGCAGAGAGACGTGAGGACCATTATGAGATGGGGGAGAGAGCTGGG 204

Qy 121 GAGTGGCCAGTTTCCATCTGTAGAACTGCCCGAGAAAGACACGGGCTTGAATGCG 180
Db 205 CAGCGGCGAGTTTGCATCTGTGCGGAAGTCCGCGACAGAGGCGACGGGCACGAGATGCGC 264

QY 181 AGCCAAAGTTCATCAAGAACGGGACGAGCCGGGCGCGGTGTGAGCCGGAGGA 240

Db 265 AGCCAAAGTTCATCAAGAACGGGCGCTGTATCAGCGCGCGGTGGGGAGAGCCGGAGGA 324

QY 241 GATCGAGCGGAGGTGAGCATCTCTCGCGAGGTGCTGCACCCAAATGTATCATCGCTTCA 300

Db 325 GATTCGAGGGGGGGGTGAGCATCTCTCGCGGAGGTATCCGGGACCCCAACATCATCACTCCCTTCA 384

301 CGCGCTATGAAACCGCACCGAGCTGTGCACATCTTGAGTAGTGTGAGAGAGA 360
 385 CCGCATTTTCGAGAAATAGACGGACCTGCTCTTATCTTGAGCTGTGAGCTCTTCTGCGGCGGCG 444

361 GCCTTCGATTTCTCTGGCCAGAGAGTCACTGATGAGAGAGGCCACCAAGCTTCAT 420

421 TAAGCAGATCCTGGATGGGGTGAACCTTCAACACAAGAAATTCCTACTTTGATCT 480

481 CAGCCGAAAACTTATGTTGTAGACAGATAATTCCCATTCACACATCAAGCTGAT 540

22 541 TGAATTGGCTGGCTCAGGAATAGAGATGGATTGAAATTTAGAGATATTTTGGAC 600

DB 625 CAGCTTCGGCATTGCGACAAAGATCGAGGCGGGGAACAGATTCAGAACATCTTCGGCAC 684

0Y 601 GCCGGAATTTGTGCTCCAGAAATTTGCACTACGAGCCCCCTGGGTCTGGAGGCTGACAT 660

Db 685 CCGGAGCTTGTGGCCCCAGAGATTGGAACATATGAGCCGCTGGGCCCTGAGAGCGGCACAT 744
 QY 661 GTGAGCATAGGCGTCATCACTTACATCCTCTTAAGTGAGAGATCCCTTTCTGGAGA 720

Db 745 GTGGAGCATGGGTGCATCACTATATCTCTGAGGGGTGCATCCCGTTCTGTGGCGA 804

Dy 721 CACGACACGAAAACTGTGGCAATATCAATCAGTGTACGACTTTGACAGAGAAATT 780

DB 805 GACCAAGCAGGAGACCGTCACCAACATCTCAGCCGCTGAACCTACGACTTCGACGAGGAGTA 864

DY 781 CTTCAGCATTACGAGCGAGCTGCGCCAAAGACTTTATTCCGAAAGCTTCTGCTTTAAGAGAC 840

Db 865 CTTGAGCAACACCGAGAGCTGSCCAAGACTTCATTCGCGCGTGTCTGTCAAGATCC 924

Qy 841 CCGAAACGGCTTCACATCCAAGAGGCTCTTCAGACACCCCTTGATATCAGCCGGT 894

Db 925 CAAGCGGAGATGACCAATTGCCGAGCCTGGAAACATTCCTGGATTAAAGCGCAT 978


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Db 633 CCCGAGTTTGTGGCCCCGAGAGATTGTAACTATGAGCGCGTGGCCCTGAGAGCGGACAT 692
Qy 661 GTGAGCATATGAGCGCTCATCACTATACCTCTTTAAGTAGAGATCCCTTTCTGGAGAG 720
Db 693 GTGAGCATCGGTGTGCATCACTATATCTCTGTAGCGGTGATCCCGTCTTGGGCGA 752
Qy 721 CACGAGCAGAGAACTGTGGCAATATATCATCACTAGTGAATTAAGATTGAGAAATT 780
Db 753 GACCAAGCAGAGAGAGCTGCTACCAACATCTCAGCCGTGAATACGACTTGAAGAGAGTA 812
Qy 781 CTTACGCATATGAGCGGAGCTGCGCAAGACCTTTATTGGAGAGCTTCTGGTTAAAGAGAC 840
Db 813 CTTAGCAACACGAGCGAGCTGGCCAGAGACTTCACTGCGGCTGTCTGTAAGATCC 872
Qy 841 CCGGAAACGCTCATCAATCAAGAGCTCTGAGACACCCCTGATCAGCGCGT 894
Db 873 CAAGCGAGATGACCATTCGCCAGAGCTGGAACATTCCTGATTAAGCGAT 926

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RESULT 9

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PCT-US02-31357-118
; Sequence 118, Application PC/TUS0231357
; GENERAL INFORMATION:
; APPLICANT: Curagen Corporation, et al
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS C
; FILE REFERENCE: 21402-462D-061
; CURRENT APPLICATION NUMBER: PCT/US02/31357
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CirusSeqList version 0.1
; SEQ ID NO 118
; LENGTH: 2132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)..(1455)
PCT-US02-31357-118

```

Query Match 29.6%; Score 515.6; DB 1; Length 2132;
 Best Local Similarity 76.1%; Pred. No. 2.8e-121;
 Matches 635; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

```

Qy 61 CATGAGCATTTCAAGCAGAGAGTGTAGAGACTTTTATGACATCGAGAGAGAGCTGGG 120
Db 93 CATGTCACGTTTACAGGAGAGAGAGTGTAGAGAGCATTATGAGAGAGAGAGAGCTGGG 152
Qy 121 GAGTGGCCAGTTTGCATCTGTGAAGAAGTCCCGGAGAGAGACAGCGGGCTTGAATATGC 180
Db 153 CAGGGCCAGTTTGGATCTGTGCGGAGAGTGCCTGGCAGAGAGAGAGAGAGAGTACGC 212

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Qy 181 AGCCAAATTTCATCAAGAGCGGAGAGCGCGGCGAGCGCGGCTGTAGCCGGAGGA 240
Db 213 AGCCAAATTTCATCAAGAGAGCGCGGCTGTTCATTCAGCGCGGCTGTAGAGAGAGGA 272
Qy 241 GATGAGGCGGAGGTGAGCATCTTCCGCGAGAGTGTGTGACCAATATGATCATCGCTGCA 300
Db 273 GATGAGGCGGAGGTGAGCATCTTCCGCGAGAGTGTGTGACCAATATGATCATCGCTGCA 332
Qy 301 CGAGCTATATGAGAACCGGACCGAGCTGTGTGATCATCTTGTAGTATGTGTGAGAGGA 360
Db 333 CGACATCTTTCAGAGAACAGAGAGAGTGTGTCTTATCTGTAGAGCTGTGTGTGTGTGAG 392
Qy 361 GCTCTTCATTTCTGTGCGCCAGAGAGTCACTGATGAGAGAGAGAGGACAGCTTCAT 420
Db 393 GCTCTTCATTTCTGTGCGGAGAGAGAGTGTGTGATGAGAGAGAGAGGACAGCTTCAT 452
Qy 421 TAAGCAGATCTGTGAGTGGGTGAATCTACCTTCAACAAGAAATTTGCTCATTTGATCT 480
Db 453 CAAGCAGATCTGTGAGCGGCTTCACTACCTGACCTTAAGCGCATTCGACACTTTGACCT 512
Qy 481 CAAGCAGAGAAACATTAATGTTTGAACAAGATATTCCTCAACATCAAGCTGAT 540
Db 513 GAGCGGAGAAACATCATGCTGTGTGAGAGAGAGTGTGTGAGAGAGAGAGAGAGCTCAT 572
Qy 541 TGACTTTGTGTGCTGCTCAGAAATGAGAGATGAGTGAATTTAAGATATTTTGGAGC 600
Db 573 CGACTTGTGAGTCCGCGACCAAGATGAGAGCGGAGAGAGAGTGAAGAAATCTTCCGAC 632
Qy 601 GCCGAAATTTGTCTCCAGAAATTTGAACTAGAGCGCTGTGAGTGTGAGCTGACAT 660
Db 633 CCCGAGTTTGTGCCCCAGAGATTTGAATGAGCGCTGTGAGCGGAGAGAT 692
Qy 661 GTGAGCATATGAGCGCTCATCACTATCTCTTAAAGTGAAGACATCCCTTCTGGAGGA 720
Db 693 GTGAGCATATGAGCGCTCATCACTATCTCTTAAAGTGAAGACATCCCTTCTGGAGGA 752
Qy 721 CACGAGCAGAGAACTGTGCAATATCATCACTAGTGAATTTAAGATTTTGTGAGAAATT 780
Db 753 GACCAAGCAGAGAGAGCTGCACCAACATCTCAGCGGTGAACATCTTGCAGAGAGAGTA 812
Qy 781 CTTAGCCATATGAGCGAGAGCTGCGCAAGAGCTTTATTTGGAAGCTTCTGTTAAAGAGAC 840
Db 813 CTTAGCAACACGAGCGAGCTGCGCAAGAGCTTATTCGCGGCTGTCTGTAAGAGATCC 872
Qy 841 CCGGAAACGCTCATCAATCCAGAGGCTCTGAGACACCCCTGTATCAGCGCGT 894
Db 873 CAAGCGAGATGACCATTCGCCAGAGCTGGAACATTCCTGATTAAGCGAT 926

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RESULT 10

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US-10-262-445-118
; Sequence 118, Application US/10262445
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catlett, Blina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Miller, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Patunrajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan

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APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYPEPTIDES ENCODING THEM AND METHODS
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 21402-462D
CURRENT APPLICATION NUMBER: US/10/262,445
CURRENT FILING DATE: 2002-10-01
PRIORITY APPLICATION NUMBER: 60/327,454
PRIORITY FILING DATE: 2001-10-05
PRIORITY APPLICATION NUMBER: 60/327,917
PRIORITY FILING DATE: 2001-10-09
PRIORITY APPLICATION NUMBER: 60/328,029
PRIORITY FILING DATE: 2001-10-09
PRIORITY APPLICATION NUMBER: 60/328,056
PRIORITY FILING DATE: 2001-10-09
PRIORITY APPLICATION NUMBER: 60/328,849
PRIORITY FILING DATE: 2001-10-12
PRIORITY APPLICATION NUMBER: 60/329,414
PRIORITY FILING DATE: 2001-10-15
PRIORITY APPLICATION NUMBER: 60/330,142
PRIORITY FILING DATE: 2001-10-17
PRIORITY APPLICATION NUMBER: 60/341,058
PRIORITY FILING DATE: 2001-10-22
PRIORITY APPLICATION NUMBER: 60/343,629
PRIORITY FILING DATE: 2001-10-24
PRIORITY APPLICATION NUMBER: 60/349,575
PRIORITY FILING DATE: 2001-10-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuroseqIst version 0.1
SEQ ID NO 118
LENGTH: 2132
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (94)..(1455)
US-10-262-445-118

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| | | | | |
|---------------------------|--------|---------------------|-----------|--------------|
| Query Match | 29.6%; | Score 515.6; | DB 8; | Length 2132; |
| Best Local Similarity | 76.1%; | Pred. No. 2.8e-121; | | |
| Matches 635; Conservative | 0; | Mismatches 199; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| Oy | 61 | CATGAGCCATTCAAGCAGCGAAGGTGGAGACTTTTATGACATCGGAGAAGAGCTGGG | 120 |
| Db | 93 | CATGCCACGTTTCAGGCAGGAGGACGTGGAGAGCACATTATGATGGGGAGAGCTGGG | 152 |
| Oy | 121 | GAGTGCCAGTTTGCATCGTAGAAGTAGTGCCTGGAGAAAGCAGCGGGCTTAGATGC | 180 |
| Db | 153 | CAGCGCCAGTTTGGGATCTGTGCGMAATGCCCGCAGAAAGGACCGGGCAGAAGATGCG | 212 |
| Oy | 181 | AGCCAAGTTTCATCAAGAGCGGCAGAGCCGGGCGAGCCGGCGGTGTGAACCGGAGGA | 240 |
| Db | 213 | AGCCAAAGTTTCATAAGAGGCCCGCCGCTGTTCATCCAGCCGGCGTGGGTGAGCGGGAGGA | 272 |
| Oy | 241 | GATCGAGCGGAGGTGAGACATCTCTCGGCAGAGTGTCTGACAACAATGTCAACGCTGCA | 300 |
| Db | 273 | GATTCAGCGGGAGGTGAACATCTCTCGGGAATCCGGACCCCAACATCATACCCTGCA | 332 |
| Oy | 301 | CGACGCTCATGAGAACCCACACCGACGATGTGACATCCCTTAGCTGTGAGGAGA | 360 |
| Db | 333 | CGACATCTTTCAGAGAACAGACGAGAGTGTCTCATCTCTGAGGTGTCTCTGGCGGGGA | 392 |
| Oy | 361 | GCTCTTCGATTTCTGTGCCCGCAGAAAGAGTCACTGATGTGAGGAGGCGCACAGCTTCAT | 420 |
| Db | 393 | GCTCTTTACITCTCGGCGGAGAAAGATCGCTGACGAGGACCAAGGACCAACCGAGTCTT | 452 |
| Oy | 421 | TAAAGAGATCCCTGATGGGGTGAATTACTTCAACAAGAAAAATTCCTCACTTGAATC | 480 |
| Db | 453 | CAGAAGATCCCTGGACGGGCTTCACTTACCTGACTCTTAAGCGCATCGACAATTGACTT | 512 |
| Oy | 481 | CAAGCCAGAAAACATATATGTTGTGACAAAGATAATTCCTCCATCCACATCAAGCTGAT | 540 |

| | | | |
|----|-----|---|-----|
| Db | 513 | GAAGCCGGAAAAATCATATGCTGCTGGACAAAGAAAGTGGCCAAACCCAGATCAAGCTCAT | 572 |
| Qy | 541 | TGACTTTGGTCTGGCTCAGCAAAATAGAGATGAGATTGAATTTTAAGATATTTTGGGAC | 600 |
| Db | 573 | CGACTTCGGCATCGCGCAACAAGATCGAGGCGGGAAACGAGTTCAAGAACATCTTTCGGCAC | 632 |
| Qy | 601 | GCCGGAATTTTGTCTCTCAGAAATTTGGAACTTAGAGGCCCTTGAGTCTTGGAAGGCTGACAT | 660 |
| Db | 633 | CCCGAGTTTGTGGCCCCCAAGATTTGGAACTTAGAGCCCTCTGAGCTTGAGGCGGACAT | 692 |
| Qy | 661 | GTGGAGCATAGGCGTCAATCACTCATCTTTAAGTGGAGCATCCCTTCTCGGAGAG | 720 |
| Db | 693 | GTGAGCATCGGTCTCATCTATATCTCTCGAGGGGTGCATCCCCGTCTCTGGGCCA | 752 |
| Qy | 721 | CACGAGCAGGAAAACTGTGGCAATATACATCAGTAGTAGTTAGACTTTGATGAGAAATT | 780 |
| Db | 753 | GACCAAGAGGAGAGCGCTCAACCAATCTCAGCGGTGAATTACGACTTCGACGAGGAGTA | 812 |
| Qy | 781 | CTTCAGCCATACGAGCGAGCTGGCCAAAGACTTTATTCCGAAGCTTCTGTATTAAGAGAC | 840 |
| Db | 813 | CTTCAGCAACACGAGCGAGCTGGCCAAAGACTTCATTCGCGGCTGCTCTCTCAAGATCC | 872 |
| Qy | 841 | CCGAAACGGCTCACTCATCCAAAGGCTCTCAGACATCCCTGATCAACGCGGAT | 894 |
| Db | 873 | CAAGGAGGAATGACATATGCCCCAGAGCTTGAACTATCTCTGATTTAAGCGAT | 926 |

RESULT 11
US-09-724-676-20895
; Sequence 20895, Application US/09724676

1 TITLE OF INVENTION: Variants of alternative splicing
2
3 FILE REFERENCE: 129181.4 Compugen
4
5 CURRENT APPLICATION NUMBER: US/09/124,676
6
7 CURRENT FILING DATE: 2000-11-28
8
9 NUMBER OF SEQ. ID NOS: 97222
10
11 SOFTWARE: PatentIn version 3.2

```

/ ORGANISM: Homo sapiens
/
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: n is a,c,g, or t
/
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (20)..(20)
/ OTHER INFORMATION: n is a,c,g, or t
/
US-09-724-676-20895

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| | | | | |
|---------------------------|-------|---------------------|-----------|--------------|
| Query Match | 29.6% | Score 51.5.4; | DB 6; | Length 2570; |
| Best Local Similarity | 76.4% | Pred. No. 3.4e-121; | | |
| Matches 633; Conservative | 0; | Mismatches 196; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|--|-----|
| QY | 61 | CATGAGCCATTTCAGACGACGAGAAAGGTGGAGACCTTTATGACATCGAGAGAGAGCTGG | 120 |
| Db | 132 | CATGTCACAGTTTCAGGCGACGAGAGACGTGGAGAGACATTATGAGATGGGGAGAGAGCTGG | 191 |
| QY | 121 | GAGTGGCCAGTTTGGCCATCTGTGAAGAGTGCCTGGGAGAGAGACGAGGCGTTTGAGTATGC | 180 |
| Db | 192 | CAGCGGCCAGTTTGGGATCTGTGGGAGAGTGCCTGGCAGAGAGGACCGGAGCAAGGATACGC | 251 |
| QY | 181 | AGCCAAATTTCATCAAGAAAGCGGACGAGCCGGGCGAGCCGGCGGGTGTAGCCGGGAGGA | 240 |
| Db | 252 | AGCCAAATTTCATCAAGAAAGCCGCCCTGTATCAAGCCGGCGTGGGGGTGAGCCGGGAGGA | 311 |
| QY | 241 | GATCGAGGGGAGGTGAGCATCTTCGGGCGAGGTCTGCACACATATGTCAATACGCTGCA | 300 |
| Db | 312 | GATCGAGGGGAGGTGAGCATCTCTCGGGAGATCTCGGCACCCCAACATCAATCACCTTCA | 371 |
| QY | 301 | CGAGCTTATAGAAACCGACCGACGTTGGTGCACATCTCTTGAGCTAGTGTCTGGAGGA | 360 |

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Db 372 CGACATCTTCAGAAACAGAGGAGTGTCTCTCATCTCGAGCTGTCTCTGGGAGG 431
Qy 361 GCTCTTCATTTCTGGGCCAGAGAGTCACTGATGAGGAGGAGGACACAGCTTAT 420
Db 432 GCTCTTACCTTCTGGGCGAGAGAGTCTGTACGAGAGGAGGAGGACACAGCTTCT 491
Qy 421 TAAGAGATCTGATGGGGTGAATACCTTTCACAAAGAAATTTGCTCACTTGTATCT 480
Db 492 CAAGCAGATCTCGAGCGGCTTCACTACCTGCACTTAAGGCGCATCGCACCTTGA 551
Qy 481 CAAGCAGAAACATTAATTTGTTAGACAGAAATTTCCATTCCACATCAAGCTGAT 540
Db 552 GAAGCGGAGAAACATCATCTGTCTGTGACAGAAACGTGCGCAACCCAGCATCAAGCTCAT 611
Qy 541 TGACTTTGCTGTGGCTCAGAAATAGAAATGAAATTAATTAATTTTGGGAC 600
Db 612 CGACTTCGGCATCGGACAGATGAGGCGGAGAACAGATTCAAGAAATCTTGGGAC 671
Qy 601 GCCGGAATTTGCTGTCCAGAAATTTGAACTACAGAGCCCTGAGCTGTGAGGCTGACAT 660
Db 672 CCCGAGTTTGTGGCCCGAGAGATTGTGAATGAGCGGCTGTGGGCTGTGAGGCGGACAT 731
Qy 661 GTGAGCATTAGGCGTCACTACCTTCTTAAAGTGAAGATCCCTTTCTGGGAGA 720
Db 732 GTGAGCATTCGCTGTCACTATCTCTCTGAGCGGTGATCCCGCTTCTGGGCGA 791
Qy 721 CACGAGAGAGAAACACTGGGAAATATCATCATGAGTTTAAAGCTTGAATGAGAAAT 780
Db 792 GACCAAGAGAGAGAGCTGACCAACATCTCAGCGGTGAATCAAGCTTGAAGAGAGTA 851
Qy 781 CTTCAGCCATACGAGCGAGCTGGCCAGAGACTTTATTCGAAAGCTTGTGTTAAAGAGAC 840
Db 852 CTTCAGCAACACAGCGAGCTGGCCAGAGACTTTCATTCGCGGCTGTCTGTCAAGATCC 911
Qy 841 CCGGAAACGGCTCACATTCAGAGGCTCTCAGACACCCCTGTGATCAG 889
Db 912 CAAGCGAGAAATGACATTCGCGCCAGAGCTGGAACATTCCTGAGTTAAG 960

RESULT 12
US-09-724-676A-20895
; Sequence 20895, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20895
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a,c,g, or t
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676A-20895

Query Match 29.6%; Score 515.4; DB 6; Length 2570;
Best Local Similarity 76.4%; Pred. No. 3.4e-121;
Matches 633; Conservativity 0; Mismatches 196; Indels 0; Gaps 0;

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Qy 61 CATGAGCATTTCAAGCAGAGAGTGAAGACTTTATGACATCGAGAGAGAGCTGGG 120
Db 132 CATGTCACGTTCAAGCAGAGAGAGTGAAGACCATTAATGAGATGGGAGAGAGCTGGG 191

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Qy 121 GAGTGGCCAGTTTGGCATCTGAAAGAAAGTCCGGGAGAGAGACAGGGGCTTGAATATGC 180
Db 192 CAGCGGCAAGTTTGGAGATCTGGGGAAGTGCCTGGGAGAAAGGAGCAGGGCAAGAGTAAGC 251
Qy 181 AGCCAAATTCTCAAGAAAGCGGAGAGCGGGGAGAGCGGGGCGGTGTGAGCTGGGAGGA 240
Db 252 AGCCAAATTCTCAAGAAAGCGGCGGCTGTCTATCCAGCGGGGAGAGAGAGCGGGAGGA 311
Qy 241 GATGAGCGGAGAGGATGACATCTGCGGAGAGTGTGTGACACCAATGTCATCAAGCTGCA 300
Db 312 GATGAGCGGAGAGGATGACATCTGCGGAGAGATCGGAGATCCGACCAATCATCATCTTGA 371
Qy 301 CGAGCTTATAGAAACCGACCGACGTGTGTGCAATCTTGAAGTGTGTGAGAGAGGA 360
Db 372 CGACATCTTCAGAAACAAAGAGAGTGTCTTATCTGAGAGTGTGTCTGTGGGGGGA 431
Qy 361 GCTCTTCATTTCTGTGGCCAGAGAGTCACTGATGAGAGAGAGGACCAAGCTTAT 420
Db 432 GCTCTTGAATCTCTGGGAGAGAGTGTGTGCGTGAAGAGAGAGAGGCGCACAGTTCT 491
Qy 421 TAAGAGATCTGGATGGGGTGAATACCTTCAACAAAGAAATTTGCTCACTTGTATCT 480
Db 492 CAAGCAGATCTCGAGCGGCTTCACTACCTGCACTTAAGCGCATCGCACCTTTGACCT 551
Qy 481 CAAGCAGAAACATTAATTTGTTAGACAGAAATTTCCATTCCACATCAAGCTGAT 540
Db 552 GAAGCGGAGAAACATCATCTGTCTGTGAGAGAGAGTGTGCCAACCAACCAAGATCAAGCTCAT 611
Qy 541 TGACTTTGCTGTGGCTCAGAAATAGAAATGAGTTGAATTTAAAGATTTTGGGAC 600
Db 612 CGACTTCGGCATTCGCGCAAGATGAGGCGGAGAACAGATTCAAGAAATCTTCTGGGAC 671
Qy 601 GCCGGAATTTGCTGTCCAGAAATTTGAACTACAGAGCCCTGAGCTGTGAGGCTGACAT 660
Db 672 CCCGAGTTTGTGGCCCGAGAGATTGTGAATGAGCGGCTGTGGGCTGTGAGGCGGACAT 731
Qy 661 GTGAGCATTAGGCGTCACTACCTTCTTAAAGTGAAGATCCCTTTCTGGGAGA 720
Db 732 GTGAGCATTCGCTGTCACTATCTCTCTGAGCGGTGATCCCGCTTCTGTGGGGA 791
Qy 721 CACGAGAGAGAAACACTGGGAAATATCATCATGAGTTTAAAGCTTGAATGAGAAAT 780
Db 792 GACCAAGAGAGAGAGCTGACCAACATCTCAGCGGTGAATCAAGCTTGAAGAGAGTA 851
Qy 781 CTTCAGCCATACGAGCGAGCTGGCCAGAGACTTTATTCGAAAGCTTGTGTTAAAGAGAC 840
Db 852 CTTCAGCAACACAGCGAGCTGGCCAGAGACTTTCATTCGCGGCTGTCTGTCAAGATCC 911
Qy 841 CCGGAAACGGCTCACATTCAGAGGCTCTCAGACACCCCTGTGATCAG 889
Db 912 CAAGCGAGAAATGACATTCGCGCCAGAGCTGGAACATTCCTGAGTTAAG 960

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RESULT 13
US-09-724-676-20893
; Sequence 20893, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20893
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:

```


Qy 601 GCCGAAATTTGTCCTCCAGAAATTTGAACTACGAGCCCTGGCTGAGAGCTGACAT 660
Db 612 CCCGAGTTTGTGGCCCCAGAGATTGTGACATAGAGCGCGCTGGAGCGGACAT 731
Qy 661 GTGAGCATAGGCGCTCATCATCTTACATCTCTTAAAGTGAGCATCCCTTCTTGGAGA 720
Db 732 GTGAGCATTCGGTGTTCATCATCTTATCTCTGAGCGGTGATCCCGTTCCTGGCGA 791
Qy 721 CACGAAAGAGGAAACACTGGGCAATATCATCATGAGTTGAGCTTGTGATGAGGAAT 780
Db 792 GACCAAGAGAGAGAGCTTCAACACATCTCAGCCGTAAGCTAGAGAGAGAGTA 851
Qy 781 CTTAGCCATACGAGCGAGCTGGCCCAAGCACTTTATTCGAACTTCTGTAAAGAGC 840
Db 852 CTTGAGCAACACAGCGAGCTGGCCAGGACTTCATTCGCGGCTGTCTGTCAAAAGATCC 911
Qy 841 CCGGAAAGGCTCACATTCGAAGAGGCTCTCAGACACCCCTGGAT 885
Db 912 CAGCGGAGAAATGACCATTTGCCAGAGCTCGAAGCATTCCTGAT 956

RESULT 15

US-10-144-771-9285
; Sequence 9285, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CU001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 9285
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-9285

Query Match

29.5%; Score 513.8; DB 8; Length 1410;
Best Local Similarity 76.2%; Pred. No. 6.9e-121;
Matches 632; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

Qy 61 CATGAGCCATTCAAGCAGACAGAGGTGAGACTTTTATGACATCGAGAGAGAGCTGG 120
Db 9 CATGTCCACATTCAAGCAGAGAGATGTTGAGGACCATTAATGAGAGAGAGAGCTTGG 68
Qy 121 GAGTGGCCAGTTTGCATCTGTGAAGAAGTCCGCGAGAAAGACGCGGCTTGAATATGC 180
Db 69 CAGTGGCCAAATTTGCCATCTGTGCGCAAGTGCAGAGGAGGACGCGGATGAGATATGC 128
Qy 181 AGCCAAGTTTCATCAAGAGCGGCAAGCGCGGCGGCGGCGGTGTGAAGCGGAGAGA 240
Db 129 AGCCAAGTTTCATCAAGAGCGGCGGCGGCGGCGGCGGCGGTGTGAAGCGGAGAGA 188
Qy 241 GATCAGCGGAGGTGAGCATCTCGGCGAGGTGCTGCAACAATGTATCATACGCTGCA 300
Db 189 GATGSAAGCGAGGTGAGCATCTCGGCGAGATCCGCCACCCCAATCATATAACTGCA 248
Qy 301 CGAGCTCTATAGAAACCGACCGAGCTGTGACATCTTGAAGTATGTCTGAGAGAGA 360
Db 249 TGACGTGTTGGAACAAGACAGATGTGTGATCTCTGAGAGTGTGTCCGTGGCGA 308
Qy 361 GCTCTTGATTTCCGCGCCAGAGAGTCACTGAGTGAAGAGAGGCCACGAGTTGAT 420
Db 309 GCTTTTCATCTTCGCGCGAGAGAGAGTCACTGAGAGTGAAGGCCACGAGTTCTT 368
Qy 421 TAAGCAGATCTGAGTGGGTGAATCTACCTTCAACAAGAAATTTGCTCACTTGTATCT 480
Db 369 CAABAATTCCTAGACGAGTGTCACTACTGTGACTCCAAAGCGCATGCACTTTGACCT 428
Qy 481 CAAAGCCAGAAACATTAATGTGTGTAGACAAAGATATTCATTCACATCAAGCTGAT 540
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Qy 541 TGACTTGTGCTGCTCAGAAATAGAGATGAGATTGAATTTAAGAAATATTTTGGAC 600
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Qy 601 GCCGAAATTTGTCCTCCAGAAATTTGAACTACGAGCCCTGGCTGAGAGCTGACAT 660
Db 549 ACCGAGTTTGTGGCCCCAGAGATGTGAATATGAGCCACTTGGCTTGAAGCTGACAT 608
Qy 661 GTGAGCATAGGCGCTCATCATCTTACATCTCTTAAAGTGAGCATCCCTTCTTGGAGA 720
Db 609 GTGAGCATTCGGTGTTCATCATCTTATCTCTGAGCGGTGATCCCGTTCCTGGCGA 780
Qy 721 CACGAAAGAGGAAACACTGGGCAATATCATCATGAGTTGAGCTTGTGATGAGGAAT 780
Db 669 GACCAAGAGAGAGAGCTTGAAGACATCTCAGCACTGAACTATGACTTTGATGAGGAAT 728
Qy 781 CTTAGCCATACGAGCGAGCTGGCCCAAGCACTTTATTCGAAAGCTTCTGTAAAGAGAC 840
Db 729 CTTGAGCAACACAGCGAGCTGGCCAGGACTTCATTCGCGAGGCTGTGTCAAAAGACCC 788
Qy 841 CCGGAAAGGCTCACATTCGAAGAGGCTCTCAGACACCCCTGGATCAG 889
Db 789 CAGAGAGAGATGACCATTCGACAGAGCTGAGCATTCCTGATCAG 837

Search completed: April 4, 2003, 22:50:26
Job time : 947.167 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 19:24:37 ; Search time 370.763 Seconds
(without alignments)
8137.548 Million cell updates/sec

Title: US-09-719-748-1_COPY_1022_1141

Perfect score: 120
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Scoring table: IDENTITY NUC
Gapop 10*0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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|------------|-------|-------------|--------|----|---------------------------------------|
| 1 | 120 | 100.0 | 454 | 16 | US-09-234-611-14012 Sequence 19174, A |
| 2 | 120 | 100.0 | 454 | 16 | US-09-235-076-19174 Sequence 19174, A |
| 3 | 120 | 100.0 | 454 | 16 | US-09-289-768-21173 Sequence 19174, A |
| 4 | 120 | 100.0 | 454 | 17 | US-09-332-782-19174 Sequence 19174, A |
| 5 | 120 | 100.0 | 454 | 29 | US-09-737-223-19174 Sequence 19174, A |
| 6 | 120 | 100.0 | 454 | 34 | US-09-804-809-14012 Sequence 19174, A |
| 7 | 120 | 100.0 | 454 | 34 | US-09-918-995-19174 Sequence 19174, A |
| 8 | 120 | 100.0 | 454 | 35 | US-09-939-397-21173 Sequence 19174, A |
| 9 | 120 | 100.0 | 480 | 29 | US-09-757-982-12 Sequence 12, Appl |
| 10 | 120 | 100.0 | 1253 | 1 | PCT-US01-08631-9265 Sequence 9265, Ap |
| 11 | 120 | 100.0 | 1451 | 16 | US-09-277-2144-176 Sequence 176, App |
| 12 | 120 | 100.0 | 1451 | 33 | US-09-891-825-176 Sequence 176, App |
| 13 | 120 | 100.0 | 1512 | 25 | US-09-649-163-7647 Sequence 7647, Ap |
| 14 | 120 | 100.0 | 1512 | 25 | US-09-652-816-8022 Sequence 8022, Ap |
| 15 | 120 | 100.0 | 1512 | 25 | US-09-652-913-8169 Sequence 8169, Ap |
| 16 | 120 | 100.0 | 1512 | 25 | US-09-652-917-2793 Sequence 2793, Ap |
| 17 | 120 | 100.0 | 1742 | 1 | PCT-US99-13411-1 Sequence 1, Appl |
| 18 | 120 | 100.0 | 1742 | 1 | PCT-US99-13411-1 Sequence 1, Appl |
| 19 | 120 | 100.0 | 1742 | 28 | US-09-719-748-1 Sequence 10, Appl |
| 20 | 120 | 100.0 | 1864 | 29 | US-09-757-982-10 Sequence 3799, Ap |
| 21 | 120 | 100.0 | 2235 | 23 | US-09-606-776-3799 Sequence 3799, Ap |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 120 100.0 2235 25 US-09-649-163-9895 Sequence 9895, Ap
23 120 100.0 2235 25 US-09-652-917-3775 Sequence 3775, Ap
24 120 100.0 2235 27 US-09-698-010-12335 Sequence 12335, A
25 120 100.0 2235 27 US-09-698-013-6041 Sequence 6041, Ap
26 109 99.2 242 11 US-08-706-765-907 Sequence 907, App
27 109 99.8 362 13 US-08-975-985-2005 Sequence 2005, Ap
28 109 90.8 362 34 US-09-912-292-30021 Sequence 30021, A
29 106 88.3 362 34 US-09-912-292-3329 Sequence 3329, Ap
30 99.2 82.7 279 20 US-09-539-806-47575 Sequence 47575, A
31 97.6 81.3 1732 80 US-09-360-207-3361 Sequence 3361, Ap
32 85.6 71.3 422 27 US-09-698-010-6454 Sequence 6454, Ap
33 80.4 67.0 495 25 US-09-652-816-4516 Sequence 4516, Ap
34 80.4 67.0 495 25 US-09-540-229-137005 Sequence 137005, Ap
35 79.4 66.2 434 21 US-09-528-409-88315 Sequence 88315, A
36 79.4 66.2 434 35 US-09-933-524-88315 Sequence 88315, A
37 79.4 66.2 434 35 US-09-933-524-88315 Sequence 88315, A
38 78.8 65.7 635 62 US-60-182-093-1080 Sequence 1080, Ap
39 78 65.0 377 21 US-09-540-766-53879 Sequence 53879, A
40 77.4 64.5 284 11 US-08-782-035-1455 Sequence 1455, Ap
41 77.4 64.5 284 21 US-08-869-540-261 Sequence 261, App
42 59 49.2 219 12 US-08-869-540-261 Sequence 261, App
43 49.2 219 45 US-60-018-911-261 Sequence 261, App
44 49.2 219 23 US-09-616-082-268 Sequence 268, App
45 58.4 48.7 332 18 US-09-411-587-970 Sequence 970, App
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ALIGNMENTS

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RESULT 1
US-09-234-611-14012
; Sequence 14012, Application US/09234611
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/234,611
; CURRENT FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14012
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-234-611-14012

Query Match 100.0%; Score 120; DB 16; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGATGAAGAAGTGCACCTGAGCCGATGAGAGCACTGTGAGTGC 60
DB 266 TCCTGATGAAGAAGTGCACCTGAGCCGATGAGAGCACTGTGAGTGC 325
QY 61 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGACACCTCC 120
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RESULT 2
US-09-235-076-19174
; Sequence 19174, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
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; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19174
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-19174

Query Match 100.0%; Score 120; DB 16; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGATGAAGAAGTGCACCTGAGCCGATGAGAGCACTGTGAGTGC 60
DB 266 TCCTGATGAAGAAGTGCACCTGAGCCGATGAGAGCACTGTGAGTGC 325
QY 61 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGACACCTCC 120
DB 326 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGACACCTCC 385
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RESULT 3
US-09-289-768-21173
; Sequence 21173, Application US/09289768
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/289,768
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21173
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-289-768-21173

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Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTGATGAAGAAGTGCACCTGAGCCGATGAGAGCACTGTGAGTGC 60
DB 266 TCCTGATGAAGAAGTGCACCTGAGCCGATGAGAGCACTGTGAGTGC 325
QY 61 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGACACCTCC 120
DB 326 ACTGAGAGAGCATCGCCAGAGAGAAAGCCCTCCACCCAGAGAGAGACACCTCC 385

RESULT 4
US-09-332-782-19174
; Sequence 19174, Application US/09332782A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/332,782A
; CURRENT FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 19174
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-332-782-19174
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Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGAGTGAC 60
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Db 266 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGAGTGAC 325
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QY 61 ACTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCAGGAGAGAGAGAGACACCTCC 120
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Db 326 ACTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCAGGAGAGAGAGAGACACCTCC 385
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RESULT 5
US-09-737-223-19174
; Sequence 19174, Application US/09737223
; GENERAL INFORMATION:
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; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/737,223
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 09/332,782
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19174
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-737-223-19174
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```
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Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGAGTGAC 60
    |||
Db 266 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGAGTGAC 325
    |||

QY 61 ACTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCAGGAGAGAGAGAGACACCTCC 120
    |||
Db 326 ACTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCAGGAGAGAGAGAGACACCTCC 385
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RESULT 6
US-09-904-809-14012
; Sequence 14012, Application US/09904809
; GENERAL INFORMATION:
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; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/904,809
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/234,611
; PRIOR FILING DATE: 1999-01-22
; NUMBER OF SEQ ID NOS: 21025
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14012
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-904-809-14012
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Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 266 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGAGTGAC 325
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QY 61 ACTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCAGGAGAGAGAGAGACACCTCC 120
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Db 326 ACTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCAGGAGAGAGAGAGACACCTCC 385
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RESULT 7
US-09-918-995-19174
; Sequence 19174, Application US/09918995
; GENERAL INFORMATION:
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; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
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; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19174
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(454)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19174
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Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 266 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGAGTGAC 325
    |||

QY 61 ACTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCAGGAGAGAGAGAGACACCTCC 120
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Db 326 ACTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCAGGAGAGAGAGAGACACCTCC 385
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RESULT 8
US-09-939-397-21173
; Sequence 21173, Application US/09939397
; GENERAL INFORMATION:
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; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/939,397
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/289,768
; PRIOR FILING DATE: 1999-04-08
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NUMBER OF SEQ ID NOS: 39996
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21173
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(454)
OTHER INFORMATION: n = A,T,C or G
US-09-939-397-21173

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Best Local Similarity 100.0%; Pred. No. 1,7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGGTGAC 60
DB 266 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGGTGAC 325
QY 61 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGGACGACCTCC 120
DB 326 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGGACGACCTCC 385

RESULT 9
US-09-757-982-12
Sequence 12, Application US/09757982
GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/757,982
CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 09/163,115
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(480)
US-09-757-982-12

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Best Local Similarity 100.0%; Pred. No. 1,7e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGGTGAC 60
DB 361 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGGTGAC 420
QY 61 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGGACGACCTCC 120
DB 421 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGGACGACCTCC 480

RESULT 10
PCT-US01-08631-9265
Sequence 9265, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 9265
LENGTH: 1253
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (231)...(1250)
OTHER INFORMATION: 100% homologous to Homo sapiens Death-associated protein
OTHER INFORMATION: kinase 2, accession number A8018001, Smith-Waterman Score=1732.
PCT-US01-08631-9265

Query Match 100.0%; Score 120; DB 1; Length 1253;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGGTGAC 60
DB 1131 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGGTGAC 1190
QY 61 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGGACGACCTCC 120
DB 1191 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGGACGACCTCC 1250

RESULT 11
US-09-277-214A-176
Sequence 176, Application US/09277214A
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE
FILE REFERENCE: MNI-079
CURRENT APPLICATION NUMBER: US/09/277,214A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 586
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 176
LENGTH: 1451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: All occurrences of n = any nucleotide
US-09-277-214A-176

Query Match 100.0%; Score 120; DB 16; Length 1451;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGGTGAC 60
DB 642 TCGCTGATGAAGAAGTGCACCTGAGCGCGATGAGACCTGAGAACTGTGAGGTGAC 701
QY 61 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGGACGACCTCC 120
DB 702 ACTGAGAGGACATCGCCGAGAGAAAGCCCTCCACCCGAGAGGAGAGGACGACCTCC 761

RESULT 12
US-09-891-825-176
Sequence 176, Application US/09891825
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE
FILE REFERENCE: MNI-079
CURRENT APPLICATION NUMBER: US/09/891,825
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US/09/277,214
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 586
SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 176
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n = any nucleotide
US-09-891-825-176
```

```
Query Match          100.0%; Score 120; DB 33; Length 1451;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TCCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTGAGGAAGTGTGAGAGTAC 60
Db 642 TCCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTGAGGAAGTGTGAGAGTAC 701
Oy 61 ACTGAGAGGACATCGCCAGAGGAAAGCCTCCACCCACGAGAGAGAGACGACACTCC 120
Db 702 ACTGAGAGGACATCGCCAGAGGAAAGCCTCCACCCACGAGAGAGAGACGACACTCC 761
```

RESULT 13

```
US-09-649-163-7647
; Sequence 7647, Application US/09649163
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Galvin, Katherine A.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Kingsbury, Gillian A.
; APPLICANT: Welch, Nadine S.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Williamson, Mark
; APPLICANT: Richardson, Jennifer
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Villevial, Jean-Luc M.G.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: Slios-Santiago, Inmaculada
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; APPLICANT: Buefield, Samantha J.
; APPLICANT: Deedes, James
; APPLICANT: Lee, John
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1164-001
; CURRENT APPLICATION NUMBER: US/09/649,163
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/150,608
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 10535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7647
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-649-163-7647
```

```
Query Match          100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TCCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTGAGGAAGTGTGAGAGTAC 60
Db 636 TCCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTGAGGAAGTGTGAGAGTAC 695
Oy 61 ACTGAGAGGACATCGCCAGAGGAAAGCCTCCACCCACGAGAGAGAGACGACACTCC 120
```

```
Db 696 ACTGAGAGGACATCGCCAGAGGAAAGCCTCCACCCACGAGAGAGAGACGACACTCC 755
```

RESULT 14

```
US-09-652-816-8022
; Sequence 8022, Application US/09652816
; GENERAL INFORMATION:
; APPLICANT: Gutierrez-Ramos, Jose-Carlos
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1177-001
; CURRENT APPLICATION NUMBER: US/09/652,816
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,111
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 9647
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8022
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-816-8022
```

```
Query Match          100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TCCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTGAGGAAGTGTGAGAGTAC 60
Db 636 TCCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTGAGGAAGTGTGAGAGTAC 695
Oy 61 ACTGAGAGGACATCGCCAGAGGAAAGCCTCCACCCACGAGAGAGAGACGACACTCC 120
Db 696 ACTGAGAGGACATCGCCAGAGGAAAGCCTCCACCCACGAGAGAGAGACGACACTCC 755
```

RESULT 15

```
US-09-652-913-8169
; Sequence 8169, Application US/09652913
; GENERAL INFORMATION:
; APPLICANT: Faib, Dean R.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1174-001
; CURRENT APPLICATION NUMBER: US/09/652,913
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,107
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 10813
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8169
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1512)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-913-8169
```

```
Query Match          100.0%; Score 120; DB 25; Length 1512;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TCCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTGAGGAAGTGTGAGAGTAC 60
Db 636 TCCTGATGAAGAAGTGCACCTGAGCCCGATGAGACCTGAGGAAGTGTGAGAGTAC 695
Oy 61 ACTGAGAGGACATCGCCAGAGGAAAGCCTCCACCCACGAGAGAGAGACGACACTCC 120
```

Db 696 ACTGAGAGSACATCGCCGAGAGAAAGCCCTCCACCCGAGGAGGAGCAGCACTCC 755

Search completed: April 4, 2003, 22:30:07
Job time : 372.763 secs

Query Match 100.0%; Score 120; DB 6; Length 1442;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAAGAAGTGTGACCTTGAGCCGGATGAGACCTTGAAGTGTGAC 60
Db 414 TCGCTGATGAAGAAGTGTGACCTTGAGCCGGATGAGACCTTGAAGTGTGAC 355
Qy 61 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCGAGAGAGACGACCTCC 120
Db 354 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCGAGAGAGACGACCTCC 295

RESULT 3

US-60-443-566-647
Sequence 647, Application US/60443566
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001447
CURRENT APPLICATION NUMBER: US/60/443,566
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 25102
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 647
LENGTH: 2085
TYPE: DNA
ORGANISM: Homo sapiens
US-60-443-566-647

Query Match 100.0%; Score 120; DB 9; Length 2085;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAAGAAGTGTGACCTTGAGCCGGATGAGACCTTGAAGTGTGAC 60
Db 1029 TCGCTGATGAAGAAGTGTGACCTTGAGCCGGATGAGACCTTGAAGTGTGAC 1088
Qy 61 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCGAGAGAGACGACCTCC 120
Db 1089 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCGAGAGAGACGACCTCC 1148

RESULT 4

US-09-539-806B-47575
Sequence 47575, Application US/09539806B
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleageane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE
FILE REFERENCE: PD-1027 CIP
CURRENT APPLICATION NUMBER: US/09/539,806B
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/706,766
PRIOR FILING DATE: September 27, 1996
PRIOR APPLICATION NUMBER: 60/004,676
PRIOR FILING DATE: October 2, 1995
PRIOR APPLICATION NUMBER: 08/749,515
PRIOR FILING DATE: November 15, 1996
PRIOR APPLICATION NUMBER: 60/006,810
PRIOR FILING DATE: November 15, 1995
PRIOR APPLICATION NUMBER: 08/822,285
PRIOR FILING DATE: March 20, 1997
PRIOR APPLICATION NUMBER: 60/013,696
PRIOR FILING DATE: March 20, 1996
PRIOR APPLICATION NUMBER: 08/951,197
PRIOR FILING DATE: October 1, 1997

PRIOR APPLICATION NUMBER: 60/027,249
PRIOR FILING DATE: October 1, 1996
PRIOR APPLICATION NUMBER: 08/826,438
PRIOR FILING DATE: March 20, 1997
PRIOR APPLICATION NUMBER: 60/016,145
PRIOR FILING DATE: April 18, 1996
Remaining Prior Application data removed - See File wrapper or PALM.
NUMBER OF SEQ ID NOS: 48372
SOFTWARE: PERL Program
SEQ ID NO 47575
LENGTH: 279

TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inctye ID No: rat0065778
FEATURE:
NAME/KEY: unsure
LOCATION: 9
OTHER INFORMATION: a, t, c, g, or other
US-09-539-806B-47575

Query Match 82.7%; Score 99.2; DB 5; Length 279;
Best Local Similarity 89.2%; Pred. No. 9.9e-19;
Matches 107; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAAGAAGTGTGACCTTGAGCCGGATGAGACCTTGAAGTGTGAC 60
Db 76 TCGCTGATGAAGAAGTGTGACCTTGAGCAAGTGAAGACCTTGAAGTGTGAC 135
Qy 61 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCGAGAGAGACGACCTCC 120
Db 136 ACGAGAGGACATTCGACGAGAGAAAGCCCTTCAACCCCGAGAGAGACGACCTCC 195

RESULT 5

US-10-144-771-3361
Sequence 3361, Application US/10144771
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: C1001321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 3361
LENGTH: 1732
TYPE: DNA
ORGANISM: HUMAN
US-10-144-771-3361

Query Match 81.3%; Score 97.6; DB 8; Length 1732;
Best Local Similarity 88.3%; Pred. No. 4e-18;
Matches 106; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 TCGCTGATGAAGAAGTGTGACCTTGAGCCGGATGAGACCTTGAAGTGTGAC 60
Db 1078 TCGCTGATGAAGAAGTGTGACCTTGAGCAAGTGAAGACCTTGAAGTGTGAC 1137
Qy 61 ACTGAGAGGACATCGCCGAGGAGAAAGCCCTCCACCGAGAGAGACGACCTCC 120
Db 1138 ACGAGAGGACATTCGACGAGAGAAAGCCCTTCAACCCCGAGAGAGACGACCTCC 1197

RESULT 6

US-10-338-044-386/c
Sequence 386, Application US/10338044
GENERAL INFORMATION:
APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur


```

; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Molecular Cardiototoxicology Modeling
; FILE REFERENCE: 44921-5090-01-US
; CURRENT APPLICATION NUMBER: US/10/338, 044
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 60/303, 819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305, 623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369, 351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377, 611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 2696
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 366
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AA892388
US-10-338-044-386
```

```

Query Match      80.7%; Score 96.8; DB 8; Length 649;
Best Local Similarity 89.7%; Pred. No. 5.6e-18;
Matches 104; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```

QY 5 TGATGAAGAAGTGTGACCTGAGGCGCGATGAGACCTGAGAACTGTGAGTGCACCTG 64
    |||||
DB 649 TGATGAAGAAGTGTGACCTGAGGCGCGATGAGACCTGAGAACTGTGAGTGCACCTG 590
    |||||
QY 65 AGGAGGACATGCCAGAGGAAAGCCCTCCACCCAGAGGAGAGACGACACTCC 120
    |||||
DB 589 AGGAGGACATGCCAGAGGAAAGCCCTCCACCCAGAGGAGAGACGACTACTCC 534
    |||||
```

```

RESULT 7
US-09-947-907-15359/c
; Sequence 15359, Application US/09947907
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: COLLECTION OF CODING REGION SINGLE
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISM (CNSP) LOCATED ON EACH OF THE HUMAN
; FILE REFERENCE: C1000896
; CURRENT APPLICATION NUMBER: US/09/947,907
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 21266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15359
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-947-907-15359
```

```

Query Match      67.0%; Score 80.4; DB 5; Length 601;
Best Local Similarity 98.8%; Pred. No. 2.4e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 39 CCTGGAAGACTGTGAGAGTGACACTGAGAGGACATCGCCAGAGAGAAAGCCCTCCACCC 98
    |||||
DB 422 CCAGAGAACTGTGAGAGTGACACTGAGAGGACATCGCCAGAGAGAAAGCCCTCCACCC 363
    |||||
QY 99 ACGGAGAGAGGACGACACTCC 120
    |||||
DB 362 ACGGAGAGAGGACGACACTCC 341
    |||||
```

```

RESULT 8
PCT-US03-01096-36
; Sequence 36, Application PC/RUS0301096
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; JONES, Antissa L.;
; APPLICANT: DAHL, Christopher R.; GIETZEN, Darryl;
; APPLICANT: CHINN, Joyce; DUFOUR, Gerard E.;
; APPLICANT: JACKSON, Jennifer L.; YU, Jimmy Y.;
; APPLICANT: TUCKSON, Olivia; YAP, Pierre B.;
; APPLICANT: AMSHEY, Stefan R.; DAM, Tam C.;
; APPLICANT: LIU, Tommy F.; GERSTIN JR., Edward H.;
; APPLICANT: PERALTA, Careyna H.; LEWIS, Samantha A.;
; APPLICANT: CHEN, Alice; MARWAHA, Rakesh;
; APPLICANT: LAN, Ruth Y.; URASHKA, Michael;
; APPLICANT: R., KRISTNAM, Sreenivasa R.; KOLLURU, Vijaykumar;
```

```

; APPLICANT: PANESAR, Iqbal S.
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1239 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/01096
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/349,384
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/349,946
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/349,413
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:7761755.9:2002JAN18
PCT-US03-01096-36
```

```

Query Match      67.0%; Score 80.4; DB 1; Length 1195;
Best Local Similarity 98.8%; Pred. No. 2.8e-13;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 39 CCTGGAAGACTGTGAGAGTGACACTGAGAGGACATCGCCAGAGAGAAAGCCCTCCACCC 98
    |||||
DB 914 CCAGAGAACTGTGAGAGTGACACTGAGAGGACATCGCCAGAGAGAAAGCCCTCCACCC 973
    |||||
```

```

QY 99 ACGGAGAGAGGACGACACTCC 120
    |||||
DB 974 ACGGAGAGAGGACGACACTCC 995
    |||||
```

```

RESULT 9
US-60-443-566-10041
; Sequence 10041, Application US/60443566
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001447
; CURRENT APPLICATION NUMBER: US/60/443,566
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 25102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10041
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-443-566-10041
```

```

Query Match      50.8%; Score 61; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

DY 60 CACTGAGGAGCATCGCCAGGAGGAACCCCTCACCACGGAGGAGGACGACCTC 119
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 CACTGAGGAGCATCGCCAGGAGGAACCCCTCACCACGGAGGAGGACGACCTC 60

| | | | |
|----|-----|---|----|
| QY | 120 | C | 12 |
| | | | |
| Db | 61 | C | 61 |

RESULT 10
US-10-266-131-2686

```

sequence 2686, application US/10266131
GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Murine Polynucleotide Tags and
TITLE OF INVENTION: Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0030-USA
CURRENT APPLICATION NUMBER: US/10/266,131
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/09/617,675
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/143,878
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 2908
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2686
LENGTH: 609
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(609)
OTHER INFORMATION: n = A,T,C or G
US-10-266-131-2686

```

| | | | | | | | |
|-----------------------|-------|------------|---------|--------|---|--------|-----|
| Query Match | 43.0% | Score | 51.6 | DB | 8 | Length | 609 |
| Best Local Similarity | 85.1% | Pred. No. | 3.5e-05 | | | | |
| Matches | 57 | Mismatches | 10 | Indels | 0 | Gaps | 0 |
| Conservative | | | | | | | |

QY 1 TCGCTGATGAAGAGGTGCACCTTGAGGCCGATAGGACCTTGAGGAACCTGTGAGAGTGC 60

D5 543 TCCCTGATGAAGAGGTACATCTGAGGACAAGCGAGGACCTTGAGGAACCTGAGAGTGC 602

| | | | |
|----|-----|---------|-----|
| QY | 61 | ACTGAGG | 67 |
| | | | |
| Db | 603 | ACAGAGG | 609 |

RESULT 11
US-10-388-360-334/C
; Sequence 334, Application US/10388360

```

1 GENERAL INFORMATION:
2 APPLICANT: GENOMIC HEALTH
3 APPLICANT: Baker, Joffe B.
4 APPLICANT: Cronin, Maureen T.
5 APPLICANT: Kiefer, Michael C.
6 APPLICANT: Shak, Steve
7 APPLICANT: Walker, Michael Graham
8 TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
9 FILE REFERENCE: 39740-0001US
10 CURRENT APPLICATION NUMBER: US/10/388,360
11 CURRENT FILING DATE: 2003-03-12
12 PRIOR APPLICATION NUMBER: US 60/412,049
13 PRIOR FILING DATE: 2002-09-18
14 PRIOR APPLICATION NUMBER: US 60/364,890
15 PRIOR FILING DATE: 2002-03-13
16 NUMBER OF SEQ. ID NOS: 384
17 SOFTWARE: FastSeq for Windows Version 4.0
18 SEQ. ID NO 334
19 LENGTH: 3373

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-334

```

| | | | | | | | |
|-----------------------|-------|--------------|------|------------|----|--------|------|
| Query Match | 27.8% | Score | 33.4 | DB | 7 | Length | 3373 |
| Best Local Similarity | 57.0% | Pred. No. | 7.2 | | | | |
| Matches | 61 | Conservative | 0 | Mismatches | 46 | Indels | 0 |
| | | | | | | Gaps | 0 |

Oy 7 ATGAAGAGGCTGCACCTTGAGGCCGGATGAGGACCTTGAAGMACTGTGAGAGTGACTGAG 66
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 ATGAAATAATGGCGCTGTGGCGGCCGAGGGGAGCCCTTAGAGGAGGCAAGCGGGGGAGGCTTCG 56

QY 67 GAGGACATCGCCAGGAGGAAGCCCTCCACCCACGGAGGAGGACAG 113
Db 55 GGTGCGCAGGAGGACGAGGCCGCTCCCGGCCGACGAGGAGAAG 9

RESULT 12
US-10-264

```

; Sequence 1083, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```

; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450

; PRIOR APPLICATION NUMBER: US 60/205,515
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 2876

```

; SEQ ID NO 1083
; LENGTH: 595
; TYPE: DNA

```

```

;
; LOCATION: 11000 bagiens
;
; FEATURE:
;
; NAME/KEY: misc_feature
;
; LOCATION: (551).(551)

```

```

;
; OTHER INFORMATION: 11 equals a,b,g, or c
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5575)..(5575)
;

```

```

;
; OTHER INFORMATION: n equals d,l,g, or c
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: {577}..{577}
;

```

```

;
; OTHER INFORMATION: n equals a,t,g, or c
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (587)..(587)
;

```

Query Match: 26.8% Score 32.
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1083

| | | |
|-----------------------|---|---------------|
| 44 | GGAACTGTGAGCTGACCTGAGGAGACATCGCCAGAGAGAAAGCCCTCCACCCACCGA | 103 |
| Best Local Similarity | 63.6% | Pred. NO. 11; |
| Matches | 49; | Conservative |
| | 0; | Mismatches |
| | 28; | Indels |
| | 0; | Gaps |

Db 463 GGAA CAGCA CGA CTGG CACA GTAG GGTCA CCG CGAG CAGCA CGG CCA GCG CACA CAGA 404

Db 403 GGATGAGCGGTCCTTC 387

RESULT 13
US-60-452-680-6448/c
; Sequence 6448, Application US/60452680

```

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew

```

```

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6448
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-452-680-6448

```

```

Query Match      26.8%; Score 32.2; DB 9; Length 891;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```

```

QY 44 GGAAGTGTGAGAGTGTGACACTGTGAGAGGACATGCGCAGAGGAAAGCCCTCCACCCACCGGA 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 GGAACAGACAGCAGCTGGCAGCTGAGAGGTTCACCGCAGCAGCAGCGCGCAGCAGACAGAGA 268
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 104 GGAGAGCAGCAGCACTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 GGATGAGCGGCTCTTC 251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 14
US-60-452-680-6447/c
; Sequence 6447, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARBIL, Michele
; APPLICANT: CARBIL, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6447
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-452-680-6447

```

```

Query Match      26.8%; Score 32.2; DB 9; Length 1160;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```

```

QY 44 GGAAGTGTGAGAGTGTGACACTGTGAGAGGACATGCGCAGAGGAAAGCCCTCCACCCACCGGA 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 715 GGAACAGACAGCAGCTGGCAGCTGAGAGGTTCACCGCAGCAGCAGCGCGCAGCAGACAGAGA 656
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 104 GGAGAGCAGCAGCACTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 GGATGAGCGGCTCTTC 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 15
US-09-620-312D-1004/c
; Sequence 1004, Application US/09620312D
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aйдong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui

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; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PF_FL_genes Version 1.0
; SEQ ID NO 1004
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(1671)
US-09-620-312D-1004

```

```

Query Match      26.8%; Score 32.2; DB 6; Length 1923;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```

```

QY 44 GGAAGTGTGAGAGTGTGACACTGTGAGAGGACATGCGCAGAGGAAAGCCCTCCACCCACCGGA 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1318 GGAACAGACAGCAGCTGGCAGCTGAGAGGTTCACCGCAGCAGCAGCGCGCAGCAGACAGAGA 1259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 104 GGAGAGCAGCAGCACTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1258 GGATGAGCGGCTCTTC 1242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: April 4, 2003, 22:50:28
Job time : 66.8335 secs

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